

GenCore version 5.1.3  
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## OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:05:45 ; Search time 364.655 Seconds

(without alignments)  
5985.683 Million cell updates/sec

Title: US-08-935-377-3

Sequence: 1 GGCCAAATGAAATTTA.....GCCCGCCGCCAACGCGCA 75

Scoring table: IDENTITY-NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

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GenEmbl:*
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_ph:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
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13: gb_un:*
14: gb_vl:*
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16: em_fun:*
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27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pin:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	75	100.0	75	6	AX326742	AX326742 Sequence
2	59	78.7	59	6	AX326760	AX326760 Sequence
3	59	78.7	59	6	AX326761	AX326761 Sequence
4	42.4	56.5	77	6	AX326768	AX326768 Sequence
5	40.6	54.1	2164	14	VH3FDPCL	X89856 V.virus DNA
6	40.6	54.1	2164	14	VH3FDPCL	X89857 V.virus DNA
7	40	53.3	84	6	A59039	A59039 Sequence 27
8	40	53.3	86	6	A59040	A59040 Sequence 28
9	39.8	53.1	78	6	AX007101	AX007101 Sequence
10	39.6	52.8	6474	6	AR105797	AR105797 Sequence
11	38.8	51.7	78	6	AX007102	AX007102 Sequence
12	38.8	51.7	5532	6	AR105803	AR105803 Sequence
13	38.4	51.2	49	6	AR105801	AR105801 Sequence
14	38.4	51.2	77	6	AR105798	AR105798 Sequence
15	38.4	51.2	6811	6	AR105798	AR105798 Sequence
16	38.2	50.9	139	6	AX003203	AX003203 Sequence
17	38.2	50.9	7252	6	AR176235	AR176235 Sequence
18	38.2	50.9	7252	6	AR176236	AR176236 Sequence
19	38.2	50.9	7387	6	AR176236	AR176236 Sequence
20	38.2	50.9	7387	6	AX007114	AX007114 Sequence
21	38	50.7	41	6	AX007114	AX007114 Sequence
22	38	50.7	51	6	AR105787	AR105787 Sequence
23	38	50.7	53	6	AR105788	AR105788 Sequence
24	38	50.7	53	6	AR105788	AR105788 Sequence
25	38	50.7	53	6	AR105788	AR105788 Sequence
26	37	49.3	69	6	AX326740	AX326740 Sequence
27	33	44.0	173811	9	AC100784	AC100784 Homo sapi
28	33	44.0	181322	9	AC027018	AC027018 Homo sapi
29	32.2	42.9	242336	2	AC097416	AC097416 Rattus no
30	32	42.7	148730	2	AC095070	AC095070 Rattus no
31	31.8	42.4	161695	2	AC079849	AC079849 Homo sapi
32	31.8	42.4	187052	2	AC078826	AC078826 Homo sapi
33	31.8	42.4	188928	9	AC020612	AC020612 Homo sapi
34	31.8	42.4	266033	2	AC009246	AC009246 Homo sapi
35	31.4	41.9	158356	2	AC108271	AC108271 Rattus no
36	31.2	41.6	147361	2	AC101893	AC101893 Mus muscu
37	31.2	41.6	162143	2	AC097553	AC097553 Rattus no
38	31.2	41.6	165563	2	AC094078	AC094078 Rattus no
39	31.2	41.3	4376	10	MUSIL13A	L13028 Mouse Inter
40	31	41.3	121121	10	AL645741	AL645741 Mouse DNA
41	31	41.3	138293	2	AC126191	AC126191 Rattus no
42	31	41.3	142732	10	AC084392	AC084392 Mus muscu
43	31	41.3	159314	2	AC126645	AC126645 Rattus no
44	31	41.3	159500	10	AC005742	AC005742 Mus muscu
45	31	41.3	237823	2	AC020886	AC020886 Mus muscu

## ALIGNMENTS

RESULT 1  
AX326742  
LOCUS AX326742 75 bp DNA Linear PAR 07-JAN-2002  
DEFINITION Sequence 3 from Patent WO0172995.  
ACCESSION AX326742  
VERSION AX326742.1 GI:18097468  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct.  
artificial sequences.  
REFERENCE  
1  
Zauderer,M. and Smith,E.S.  
METHODS OF PRODUCING A LIBRARY AND METHODS OF SELECTING  
POLYNUCLEOTIDES OF INTEREST  
Patent: WO 01/72995-A 3 04-OCR-2001;  
JOURNAL

UNIVERSITY OF ROCHESTER (US)  
Location/Qualifiers  
1..75  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Nucleotide Sequence of pEL/tk"

BASE COUNT 19 a 16 c 19 g 21 t  
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Best Local Similarity 100.0%; Pred. No. 1.5e-12;  
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGGCAAAATTTGAATTTATTTTGGAAATATAAGCGCCGCATGGCCGC 60  
Qy 61 GCGGCCAAGCGCGGA 75  
Db 61 GCGGCCAAGCGCGGA 75

RESULT 2  
LOCUS AX326760 59 bp DNA linear PAT 07-JAN-2002  
DEFINITION Sequence 21 from Patent W00172995.  
ACCESSION AX326760  
VERSION AX326760.1 GI:18097479  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 Zauderer, M. and Smith, E.S.  
TITLES Methods of producing a library and methods of selecting polynucleotides of interest  
JOURNAL Patent: WO 0172995-A 21 04-OCT-2001;  
UNIVERSITY OF ROCHESTER (US)  
FEATURES  
source Location/Qualifiers  
1..59  
/organism="synthetic construct"  
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/note="Synthetic EL promoter MM438"

BASE COUNT 16 a 10 c 12 g 21 t  
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Best Local Similarity 100.0%; Pred. No. 1e-07;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCAAAATTTGAATTTATTTTGGAAATATAAGCGCCGCATGGCCGC 59  
Db 1 GGGCAAAATTTGAATTTATTTTGGAAATATAAGCGCCGCATGGCCGC 59

RESULT 3  
LOCUS AX326761 59 bp DNA linear PAT 07-JAN-2002  
DEFINITION Sequence 22 from Patent W00172995.  
ACCESSION AX326761  
VERSION AX326761.1 GI:18097480  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 Zauderer, M. and Smith, E.S.  
TITLES Methods of producing a library and methods of selecting polynucleotides of interest  
JOURNAL Patent: WO 0172995-A 22 04-OCT-2001;  
UNIVERSITY OF ROCHESTER (US)  
FEATURES  
source Location/Qualifiers  
1..59

/organism="synthetic construct"  
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BASE COUNT 21 a 12 c 10 g 16 t  
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Query Match 78.7%; Score 59; DB 6; Length 59;  
Best Local Similarity 100.0%; Pred. No. 1e-07;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AAAAATTTGAATTTATTTTGGAAATATAAGCGCCGCATGGCCGC 63  
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RESULT 4  
LOCUS AX326768 77 bp DNA linear PAT 07-JAN-2002  
DEFINITION Sequence 29 from Patent W00172995.  
ACCESSION AX326768  
VERSION AX326768.1 GI:18097486  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 Zauderer, M. and Smith, E.S.  
TITLES Methods of producing a library and methods of selecting polynucleotides of interest  
JOURNAL Patent: WO 0172995-A 29 04-OCT-2001;  
UNIVERSITY OF ROCHESTER (US)  
FEATURES  
source Location/Qualifiers  
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/db\_xref="taxon:32630"  
/note="Elova"

BASE COUNT 29 a 7 c 11 g 30 t  
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Query Match 56.5%; Score 42.4; DB 6; Length 77;  
Best Local Similarity 97.7%; Pred. No. 0.011;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGGCAAAATTTGAATTTATTTTGGAAATATAAGC 44  
Db 1 GGGCAAAATTTGAATTTATTTTGGAAATATAAGC 44

RESULT 5  
LOCUS VWH3FDPCL 2164 bp DNA linear VRL 03-JAN-1996  
DEFINITION V. virus DNA for Hind III F fragment (clone VDPCL).  
ACCESSION X89856  
VERSION X89856.1 GI:927568  
KEYWORDS HindIII F fragment; hph gene; hygromycin phosphotransferase; promoter.  
SOURCE Vaccinia virus.  
ORGANISM Vaccinia virus.  
REFERENCE 1 (bases 1 to 2164)  
TITLES Pfleiderer, M., Falkner, F.G. and Dörner, F.  
A novel vaccinia virus expression system allowing construction of recombinants without the need for selection markers, plasmids and bacterial hosts  
JOURNAL J. Gen. Virol. 76 (Pt 12), 2957-2962 (1995)  
MEDLINE 96112180  
PUBMED 8847500  
REFERENCE 2 (bases 1 to 2164)  
TITLES Pfleiderer, M.  
Direct Submission  
JOURNAL Submitted (20-JUL-1995) M. Pfleiderer, Immuno AG, A. 2304 Orth/Donau, Uferstrasse 15, AUSTRIA

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COMMENT      Related sequence M35027.
FEATURES
  Source      Location/Qualifiers
              1..2164
                /organism="Vaccinia virus"
                /strain="WR"
                /specific_host="mammalians"
                /db_xref="taxon:10245"
                /map="45478 nt number"
                /clone="VDPc 1"
                /cell_line="recombinant Vaccinia virus"
                /lab_host="mammalian cell lines"
  misc_feature 1..485
    /note="Hind III F fragment"
  misc_feature 479..1662
    /note="NOT I gene cassette"
  misc_feature 479
    /note="NOT I cleavage site corresponding to the unique NOT
    I site in the Vv genome at position 45478 (strain
    copenhagen)"
  promoter      486..543
    /note="strong synthetic early/late promoter"
  misc_feature 536
    /note="unique sfi I cleavage site"
  promoter      544..594
    /note="weak synthetic early/late promoter"
  gene          595..1620
    /gene="hph"
    /gene="hph"
    /gene="hph"
  CDS           595..1620
    /gene="hph"
    /codon_start=1
    /product="hygromycin phosphotransferase"
    /protein_id="CAA61952.1"
    /db_xref="GI:953210"
    /translation="MKKPELTATSVKFLIEKFDVSVDLMQISEGESRAFSFDVGR
    GYLRVNSCADGFYKDRVYRHFASALPIPEVLIDIGEFSESLTICISRRAGVTLDD
    LPETELPAVLQPVAFAMDAIAADLSOTSGFGPGGTCGTTWRDIFCAIDPHY
    HMOTVMDTVASASVAQALDELMAEDCEPVRHLVHADFGSNVLTIDNGRTTAVIDMS
    EMFQGSQYEVANIEFWRPWLACMEQOTRFERRHPLAGSPRLRAYMLRTIGLDQLYQ
    SLVDGNFDDAAMAAGRCDAIVRSAGTGVGTQIARRSAVAWTDGCEVLADSGNRRPS
    TRPRAKE"
  misc_feature 1635
    /note="Rsr II cleavage site"
  misc_feature 1642
    /note="NOT I cleavage site"
  misc_feature 1643..2164
    /note="Hind III F fragment"
  BASE COUNT  586 a 488 c 475 g 615 t
  ORIGIN
Query Match      54.1%; Score 40.6; DB 14; Length 2164;
Best Local Similarity 73.2%; Pred. No. 0.061;
Matches 52; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 5 AAAAATTGAATTTATTTTGGAAATATAAGCGCCCGCATGGCCCGCGCC 64
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DB 488 AAAAATTGAATTTATTTTGGAAATATAAGCGCCCGCATATG 547

OY 65 CCAACGCGGA 75
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DB 548 TAAAGTTGAA 558

RESULT 6
VH3FDPc2/c 2164 bp DNA linear VRL 03-JAN-1996
LOCUS      VH3FDPc2
DEFINITION V.virus DNA for Hind III F fragment (clone VDPc2).
ACCESSION  X89857.1
VERSION    X89857.1 GI:927569
KEYWORDS   HindIII F fragment; hph gene; hygromycin phosphotransferase;
            promoter.
SOURCE      Vaccinia virus.
ORGANISM   Vaccinia virus

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REFERENCE
  AUTHORS    Orthopoxvirus.
  TITLE      1 (bases 1 to 2164)
  JOURNAL    J. Gen. Virol. 76 (Pt 12), 2957-2962 (1995)
  MEDLINE    96112180
  PUBMED     8847500
  REFERENCE 2 (bases 1 to 2164)
  AUTHORS    Pfeleiderer, M.
  TITLE      A novel Vaccinia virus expression system allowing construction of
  JOURNAL    recombinants without the need for selection markers, plasmids and
              bacterial hosts
  JOURNAL    Submitted (20-JUL-1995) M. Pfeleiderer, Immuno AG, A. 2304
  TITLE      Orth/Donau, Uferstrasse 15, AUSTRIA
  COMMENT    Related sequence M35027.
  FEATURES
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                  /organism="Vaccinia virus"
                  /strain="WR"
                  /specific_host="mammalians"
                  /db_xref="taxon:10245"
                  /map="45478 nt number"
                  /clone="VDPc 2"
                  /cell_line="recombinant Vaccinia virus"
                  /lab_host="Mammalian cell lines"
                  1..485
                    /note="Hind III F fragment"
                    /complement(479..1642)
                    /note="NOT I gene cassette"
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                      /note="NOT cleavage site corresponding to the unique NOT I
                      site in the Vv genome at position 45478 (strain
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                        /note="Rsr II cleavage site"
                        /complement(506..1531)
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                        /complement(506..1531)
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                        /protein_id="CAA61953.1"
                        /db_xref="GI:953211"
                        /translation="MKKPELTATSVKFLIEKFDVSVDLMQISEGESRAFSFDVGR
                        GYLRVNSCADGFYKDRVYRHFASALPIPEVLIDIGEFSESLTICISRRAGVTLDD
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                        HMOTVMDTVASASVAQALDELMAEDCEPVRHLVHADFGSNVLTIDNGRTTAVIDMS
                        EMFQGSQYEVANIEFWRPWLACMEQOTRFERRHPLAGSPRLRAYMLRTIGLDQLYQ
                        SLVDGNFDDAAMAAGRCDAIVRSAGTGVGTQIARRSAVAWTDGCEVLADSGNRRPS
                        TRPRAKE"
                        complement(1532..1585)

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      /complement(1598..1639)
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        /note="NOT I cleavage site"
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Query Match      54.1%; Score 40.6; DB 14; Length 2164;
Best Local Similarity 73.2%; Pred. No. 0.061;
Matches 52; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 5 AAAAATTGAATTTATTTTGGAAATATAAGCGCCCGCATGGCCCGCGCC 64
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DB 1638 AAAAATTGAATTTATTTTGGAAATATAAGCGCCCGCATATG 1579

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OY 65 CCACGCGCGA 75  
Db 1578 TAAAGTTGAA 1568

RESULT 7  
LOCUS A59039 84 bp DNA linear PAT 06-MAR-1998  
DEFINITION Sequence 27 from Patent EP0753581.  
ACCESSION A59039  
VERSION A59039.1 GI:3714474  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 84)  
AUTHORS Scheiflinger, F.D., Antoine, G.D., Falkner, Falko-Guenther, D.,  
Dorner, F.P. and Eibl, J.D.  
TITLE Improved recombinant eukaryotic cytoplasmic viruses, method for  
their production and their use as vaccines  
JOURNAL Patent: EP 0753581-A 27 15-JAN-1997;  
IMMUNO AG (AT)

FEATURES  
source Location/Qualifiers  
BASE COUNT 28 a 8 c 10 g 38 t  
ORIGIN  
Query Match 53.3%; Score 40; DB 6; Length 84;  
Best Local Similarity 82.1%; Pred. No. 0.059;  
Matches 46; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCAAAATGAAATTTATTTTGGATATATAAGCGCGCCATGGGCC 58  
Db 9 CTTAAATGAAATTTATTTTGGATATATAAATAGGCTTCATGGCC 64

RESULT 8  
LOCUS A59040 86 bp DNA linear PAT 06-MAR-1998  
DEFINITION Sequence 28 from Patent EP0753581.  
ACCESSION A59040  
VERSION A59040.1 GI:3714475  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 86)  
AUTHORS Scheiflinger, F.D., Antoine, G.D., Falkner, Falko-Guenther, D.,  
Dorner, F.P. and Eibl, J.D.  
TITLE Improved recombinant eukaryotic cytoplasmic viruses, method for  
their production and their use as vaccines  
JOURNAL Patent: EP 0753581-A 28 15-JAN-1997;  
IMMUNO AG (AT)

FEATURES  
source Location/Qualifiers  
BASE COUNT 38 a 11 c 9 g 28 t  
ORIGIN  
Query Match 53.3%; Score 40; DB 6; Length 86;  
Best Local Similarity 82.1%; Pred. No. 0.059;  
Matches 46; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 3 CCAAAATGAAATTTATTTTGGATATATAAGCGCGCCATGGGCC 58  
Db 80 CTTAAATGAAATTTATTTTGGATATATAAATAGGCTTCATGGCC 25

RESULT 9  
AX007101/c

LOCUS AX007101 78 bp DNA linear PAT 06-SEP-2000  
DEFINITION Sequence 1 from Patent EP0972840.  
ACCESSION AX007101  
VERSION AX007101.1 GI:9994992  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 78)  
AUTHORS Barcena, D.R., Parra, F.F., Blasco, L.R., Morales, C.M., Pages, M.A.,  
Sanchez, V.J., Torres, T.J., and Vazquez, R.B.  
TITLE New attenuated myxoma recombinant virus and its use in the  
preparation of mixed vaccines against myxomatosis and rabbit  
hemorrhagic disease  
JOURNAL Patent: EP 0972840-A 1 19-JAN-2000;  
INST NAC INVEST TECN AGR ALIM (ES); FUNDACION PARA EL ESTUDIO Y DE  
(ES)

FEATURES  
source Location/Qualifiers  
BASE COUNT 30 a 13 c 9 g 26 t  
ORIGIN  
Query Match 53.1%; Score 39.8; DB 6; Length 78;  
Best Local Similarity 86.3%; Pred. No. 0.067;  
Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 5 AAAAATGAAATTTATTTTGGATATATAAGCGCGCCATGG 55  
Db 54 AAAAATGAAATTTATTTTGGATATATAAATAGCGAGATGG 4

RESULT 10  
LOCUS AR105797 6474 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 66 from patent US 6103244.  
ACCESSION AR105797  
VERSION AR105797.1 GI:12819862  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 6474)  
AUTHORS Dorner, F., Scheiflinger, F., Falkner, F., Gunter, and Pfeleiderer, M.  
TITLE Methods for generating immune responses employing modified vaccinia  
of fowlpox viruses  
JOURNAL Patent: US 6103244-A 66 15-AUG-2000;  
LOCATION/Qualifiers  
source 1. 6474  
BASE COUNT 1649 a 1533 c 1411 g 1881 t  
ORIGIN  
Query Match 52.8%; Score 39.6; DB 6; Length 6474;  
Best Local Similarity 83.3%; Pred. No. 0.14;  
Matches 45; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 5 AAAAATGAAATTTATTTTGGATATATAAGCGCGCCATGGGCC 58  
Db 3964 AAAAATGAAATTTATTTTGGATATATAAATAGGCTTCATGGCC 3911

RESULT 11  
AX007102 78 bp DNA linear PAT 06-SEP-2000  
LOCUS AX007102  
DEFINITION Sequence 2 from Patent EP0972840.  
ACCESSION AX007102  
VERSION AX007102.1 GI:9994993  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct.  
synthetic construct.



artificial sequences.  
1 (bases 1 to 78)  
AUTHORS Barcena,D.R., Parra,F.F., Blasco,L.R., Morales,C.M., Pages,M.A., Sanchez,V.J., Torres,T.J. and Vazquez,R.B.  
TITLE New attenuated myxoma recombinant virus and its use in the preparation of mixed vaccines against myxomatosis and rabbit hemorrhagic disease  
JOURNAL Patent: EP 0972840-A 2 19-JAN-2000;  
INST NAC INVEST TECN AGR ALIM (ES); FUNDACION PARA EL ESTUDIO Y DE (ES)  
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/db\_xref="taxon:32630"  
/note="Early/Late promoter"  
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Best Local Similarity 86.0%; Pred. No. 0.13;  
Matches 43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 5 AAAAAATTGAATTTATTTTGTGGAATATAAGCGGCCCATG 54  
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Db 29 AAAAAATTGAATTTATTTTGTGGAATATAAATACGACATG 78  
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RESULT 12  
LOCUS AR105803 5532 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 72 from patent US 6103244.  
ACCESSION AR105803  
VERSION AR105803.1 GI:12819868  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5532)  
AUTHORS Dörner,F., Schefflinger,F., Falkner,F.Günter. and Pfeleiderer,M.  
TITLE Methods for generating immune responses employing modified vaccinia of fowlpox viruses  
JOURNAL Patent: US 6103244-A 72 15-AUG-2000;  
FEATURES  
source 1..5532  
/organism="unknown"  
BASE COUNT 1482 a 1326 c 1263 g 1461 t  
ORIGIN

Query Match 51.7%; Score 38.8; DB 6; Length 5532;  
Best Local Similarity 79.3%; Pred. No. 0.24;  
Matches 46; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 3 CCAAAATGAAATTTATTTTGTGGAATATAAGCGGCCCATG 60  
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Db 3709 CTAATAATGAAATTTATTTTGTGGAATATAAAGCGCTCATGAGCG 3652  
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RESULT 13  
LOCUS AR105801 49 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 70 from patent US 6103244.  
ACCESSION AR105801  
VERSION AR105801.1 GI:12819866  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 49)  
AUTHORS Dörner,F., Schefflinger,F., Falkner,F.Günter. and Pfeleiderer,M.  
TITLE Methods for generating immune responses employing modified vaccinia of fowlpox viruses  
JOURNAL Patent: US 6103244-A 70 15-AUG-2000;  
FEATURES  
Location/Qualifiers

source 1..49  
/organism="unknown"  
BASE COUNT 18 a 1 c 5 g 25 t  
ORIGIN

Query Match 51.2%; Score 38.4; DB 6; Length 49;  
Best Local Similarity 97.5%; Pred. No. 0.17;  
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCAAAATGAAATTTATTTTGTGGAATATAA 42  
|||||  
Db 9 CTAATAATGAAATTTATTTTGTGGAATATAA 48  
|||||

RESULT 14  
LOCUS AX326769 77 bp DNA linear PAT 07-JAN-2002  
DEFINITION Sequence 30 from Patent WO0172995.  
ACCESSION AX326769  
VERSION AX326769.1 GI:18097487  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Zauderer,M. and Smith,E.S.  
TITLE Methods of producing a library and methods of selecting polynucleotides of interest  
JOURNAL Patent: WO 0172995-A 30 04-OCT-2001;  
UNIVERSITY OF ROCHESTER (US)  
FEATURES  
source 1..77  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Elovarv"  
BASE COUNT 30 a 11 c 7 g 29 t  
ORIGIN

Query Match 51.2%; Score 38.4; DB 6; Length 77;  
Best Local Similarity 97.5%; Pred. No. 0.18;  
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AAAAAATGAAATTTATTTTGTGGAATATAAGC 44  
|||||  
Db 77 AAAAAATGAAATTTATTTTGTGGAATATAAGC 38  
|||||

RESULT 15  
LOCUS AR105798 6811 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 67 from patent US 6103244.  
ACCESSION AR105798  
VERSION AR105798.1 GI:12819863  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 6811)  
AUTHORS Dörner,F., Schefflinger,F., Falkner,F.Günter. and Pfeleiderer,M.  
TITLE Methods for generating immune responses employing modified vaccinia of fowlpox viruses  
JOURNAL Patent: US 6103244-A 67 15-AUG-2000;  
FEATURES  
source 1..6811  
/organism="unknown"  
BASE COUNT 1923 a 1567 c 1486 g 1835 t  
ORIGIN

Query Match 51.2%; Score 38.4; DB 6; Length 6811;  
Best Local Similarity 97.5%; Pred. No. 0.33;  
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCAAAATGAAATTTATTTTGTGGAATATAA 42

DB 4988 CTAATAATTGAAATTTTATTTTGGGAATATA 4949

Search completed: November 10, 2002, 06:52:46  
Job time : 369.655 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:42:15 ; Search time 675 Seconds

(without alignments)  
1799.499 Million cell updates/sec

Title: US-08-935-377-3

Perfect score: 1 GGCCTAAATGAAATTTTA.....GCCCGGCGCCCAACGGCGGA 75

Sequence: IDENTITY\_NUC

Scoring table: Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

EST: \*  
1: em\_estda: \*  
2: em\_esthum: \*  
3: em\_estlin: \*  
4: em\_estmu: \*  
5: em\_estov: \*  
6: em\_estpl: \*  
7: em\_estro: \*  
8: em\_hlc: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_hlc: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estfun: \*  
16: em\_estom: \*  
17: gb\_gss: \*  
18: em\_gss\_hum: \*  
19: em\_gss\_inv: \*  
20: em\_gss\_pln: \*  
21: em\_gss\_vit: \*  
22: em\_gss\_fun: \*  
23: em\_gss\_mam: \*  
24: em\_gss\_mus: \*  
25: em\_gss\_other: \*  
26: em\_gss\_pro: \*  
27: em\_gss\_rtd: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	35.4	47.2	1201	17	CNS01651
2	33.4	44.5	158	10	AM297017 UI-H-BW0-
3	33.4	44.5	453	14	BM988219 UI-H-COO-
4	33	44.0	164	10	BE075111 PM1-BT058
5	32.2	42.9	1267	14	BO955325 AGENCOURT
6	31.8	42.4	586	14	BO578952 WHE2963_F

7	31.6	42.1	261	10	AM750324
c 8	31.6	42.1	962	12	BE177217
c 9	31.2	41.6	484	13	BE1798613
c 10	31.2	41.6	501	10	AM515378
c 11	31	41.3	581	17	A2305110
12	31	41.3	602	17	A2989344
c 13	30.8	41.1	371	12	BE916182
c 14	30.6	40.8	1101	17	CNS00YWS
15	30.4	40.5	381	13	BM054767
16	30.4	40.5	909	17	A0743767
17	30.2	40.3	703	13	BM382516
18	30.2	40.3	500	14	BO580344
19	30.2	40.3	797	17	BM155494
20	30	40.0	347	10	BE075085
21	30	40.0	607	9	AI570555
c 22	30	40.0	790	12	BE211548
c 23	30	40.0	872	17	A0752434
c 24	30	40.0	1437	14	BO962773
25	29.8	39.7	431	10	AM947829
26	29.8	39.7	812	12	BE969600
c 27	29.8	39.7	1011	14	BM808393
c 28	29.8	39.7	1404	9	AI964281
c 29	29.6	39.5	470	13	BI349738
c 30	29.6	39.5	750	12	BE540838
c 31	29.6	39.5	829	13	BM393275
c 32	29.6	39.5	829	13	BM395278
c 33	29.6	39.5	932	10	AM730732
c 34	29.6	39.5	966	17	BM133169
35	29.6	39.5	1035	14	BO735369
36	29.4	39.2	419	10	AM753884
c 37	29.4	39.2	468	10	AM297722
c 38	29.4	39.2	818	12	BE613522
c 39	29.4	39.2	1003	13	BM474859
c 40	29.2	38.9	230	9	AA339067
c 41	29.2	38.9	302	17	CNS03AZD
c 42	29.2	38.9	459	13	BM396122
c 43	29.2	38.9	617	10	AV645827
c 44	29.2	38.9	644	9	AI902252
c 45	29.2	38.9	1018	13	BM393128

## ALIGNMENTS

RESULT 1  
CNS01651/c  
LOCUS  
DEFINITION  
Drosophila melanogaster genome survey sequence T7 end of BAC  
BACN15M07 of DrosBAC library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.

ACCESSION  
AL106303  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

## COMMENT

Submitted (23-JUL-1999) Genoscope - Centre National de Séquençage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a  
collaboration with the European Drosophila Genome Project (EDGP) -  
http://www.edgp.ebi.ac.uk. This Drosophila melanogaster BAC  
library (Dros-BAC) was made by Alain Billard at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MRC  
project grant. The DNA was prepared from embryos by Alain Boucheton  
and Genevieve Payan. It has been constructed in the vector  
pBelobAC11.

## FEATURES

Location/Qualifiers

RESULT 2	
AM297017	
LOCUS	158 bp mRNA linear EST 16-JAN-2000
DEFINITION	UT-H-BM0-a.jf-d-09-0-U1.s1 NC1.CGAP-Sub6 Homo sapiens cDNA clone IMAGE:2731457 3, mRNA sequence.
ACCESSION	AM297017
VERSION	AM297017.1 GI:6703653
KEYWORDS	EST.
SOURCE	human.

```

FEATURES
source
location/Qualifiers
1..158
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2731457"
/clone_id="NCI_CGAP_Sub6"
/lab_host="DH10B (Life Technologies)"
/vector="pTR73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub6
is a subtracted library derived from BW, which consists
of a mixture of four normalized libraries: NCI_CGAP_Brn50,
NCI_CGAP_Lu13, NCI_CGAP_Ov18, GBC1. The NCI_CGAP_Sub6
library had 7 million recombinants. A single-stranded DNA
preparation of BW was used as a tracer in a subtractive
hybridization with a driver comprising: the IMAGE pool
(NCI_CGAP_Ki13 pool 1 LLM4 3334-3337, 3682-3683,
3798-3803 (IMAGE Clonoids 1322376-133911,
1456008-1456775, 1500552-1502855); NCI_CGAP_Ki45 pool 1
LLM4 3338-3342, 3722-3725, 3776-3778 (IMAGE Clonoids
1333912-1325831, 1471368-1472903, 1492104-1493255);

```

[illegible]

FEATURES	Location/Qualifiers
source	1. .453

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/organism="Homo sapiens"
/ab_xref="taxon:9606"
/clone_image="5861931"
/clone_lib="MCI-CGAP-Sub9"
/rnause_type="mixed"
/dev_stage="mixed"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT73-Pac (Pharmacia) with a modified

```

polylinker: Site.1: EcoR I; Site.2: Not I; tissues:  
Cholonic mucosa with Crohns disease, Cholonic mucosa with  
ulcerative colitis, Fetal thymus, Cervix, Cervical  
adenosquamous carcinoma, Ligament cells, Prostate  
carcinoma, Bladder carcinoma, Brain oligodendrocyte  
NCLCAP-Sub9 is a substracted cDNA library constructed  
according to Bonaldo, Lennon and Soares, Genome Research,  
6:791-806, 1996. First strand cDNA synthesis was primed  
with an oligo-dT primer containing a Not I site. Double  
stranded cDNA was ligated to an EcoR I adaptor, digested  
with Not I, and cloned directionally into pMT73-Pac  
vector. The oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tags for this library are CGTC, AACG, GGGCC,  
GGAGG, TAGC, TAAGC, ATGCG, AGACA, ATCAC. For additional  
information, contact: Bento Soares, bento-soares@uiova.edu  
TAG-LIB=UI-H-COD  
TAG-TISSUE=Cervical Adenosquamous Carcinoma  
TAG\_SEQ=CGAAG

BASE COUNT 63 a 169 c 148 g 73 t

ORIGIN

Query Match 44.5%; Score 33.4; DB 14; Length 453;  
Best Local Similarity 72.9%; Pred. No. 9.4e+02;  
Matches 43; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 16 TTTTATTTTTTTTTCGATATTAAGCGCGCCGCGCCGACGCGG 74  
|||||TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT  
Db 2 TTTTATTTTTTTTTCGATATTAAGCGCGCGCCGCGCCGACGCGG 60

RESULT 4  
LOCUS BE075111 164 bp mRNA linear EST 09-JUN-2000  
DEFINITION PM1-BT0585-110200-003-h11 BT0585 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BE075111  
VERSION BE075111.1 GI:8423655  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 164)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
CONTACT: Simpson A.J.G.  
LABORATORY of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6tz=PM1-BT0585-110  
200-003-h11&t3=2000-02-11&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 127.  
Location/Qualifiers  
1..164  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="BT0585"

/dev.stgce="Adult"  
/note="Organ: breast; Vector: puc18; Site.1: SmaI; Site.2:  
SmaI; A mini-library was made by cloning products derived  
from OESTES PCR (U.S. Letters Patent application No. 196  
716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."

BASE COUNT 51 a 32 c 22 g 59 t

ORIGIN

Query Match 44.0%; Score 33; DB 10; Length 164;  
Best Local Similarity 79.6%; Pred. No. 2.2e+03;  
Matches 39; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 5 AAAAATGAAATTTTATTTTTCGATATTAAGCGCGCCGACAT 53  
|||||TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT  
Db 103 AAGAGAGAAATTTTTCGATATTAAGCGCGCCGACAT 151

RESULT 5  
LOCUS B0955325/c 1267 bp mRNA linear EST 21-AUG-2002  
DEFINITION AGENCOURT\_8864016 NIH\_MGC\_129 Mus musculus cDNA clone IMAGE:6311745  
ACCESSION B0955325  
VERSION B0955325.1 GI:22370803  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1267)  
AUTHORS NIH-MGC http://imgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Susan L. Sullivan, PhD.  
CDNA Library Preparation: Resgen, Invitrogen Corp.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLM13736 row: c column: 10  
High quality sequence stop: 86  
High quality sequence start: 571.  
Location/Qualifiers  
1..1267  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
/clone\_lib="IMAGE:6311745"  
/clone\_lib="NIH\_MGC\_129"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: olfactory epithelium; Vector:  
pCMV-SPORT6.1.ccd; Site.1: EcoRV; Site.2: NotI. Cloned  
unidirectionally. Primer: Oligo dT. Average insert size  
2.2 kb. Constructed by Resgen, Invitrogen Corp. Note: this  
is a NIH-MGC Library."

BASE COUNT 258 a 391 c 360 g 253 t 5 others

ORIGIN

Query Match 42.9%; Score 32.2; DB 14; Length 1267;  
Best Local Similarity 70.5%; Pred. No. 8.3e+02;  
Matches 43; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

OY 1 GGGCAAAATTTGAATTTTTCGATATTAAGCGCGCCGACATGGGCGG 60  
|||||TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT  
Db 807 GGGCAAAATTTGAAGGCTTTTTCGATATTAAGCGCGCCGACGAG 748  
OY 61 G 61

Db 747 G 747

RESULT 6  
LOCUS B0578952  
DEFINITION B0578952 586 bp mRNA linear EST 19-JUN-2002  
WHE2963\_F04\_K07ZS wheat dormant embryo cDNA library Trilicium  
aestivum cDNA clone WHE2963\_F04\_K07, mRNA sequence.  
B0578952  
ACCESSION B0578952.1 GI:21482269  
VERSION B0578952.1  
KEYWORDS  
SOURCE bread wheat  
ORGANISM Trilicium aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae  
; Trilicaceae; Trilicium.  
1 (bases 1 to 586)  
REFERENCE Anderson,O.D., Chao,S., Chin,A., Close,T.J., Doherty,L., Fenton  
AUTHORS ,R.D., Iazo,G.R., Nausch,C.J., Walker-Simmons,M.K. and Wilson,C.  
TITLE The structure and function of the expressed portion of the wheat  
genomes - Dormant embryo cDNA library  
JOURNAL Unpublished (2001)  
COMMENT Contact: Olin Anderson  
US Department of Agriculture, Agriculture Research Service, Pacific  
West Area, Western Regional Research Center  
800 Buchanan Street, Albany, CA 94710, USA  
Tel: 5105595773  
Fax: 5105595818  
Email: oanderson@w.usda.gov  
Sequences have been trimmed to remove vector sequence and low  
quality sequence with phred score less than 20  
Seq primer: SK primer.  
Location/Qualifiers  
1..586  
/organism="Trilicium aestivum"  
/cultivar="Brevor"  
/db\_xref="taxon:4565"  
/clone\_lib="WHE2963\_F04\_K07"  
/clone\_lib="Wheat dormant embryo cDNA library"  
/tissue\_type="Seed embryo"  
/dev\_stage="Mature seed"  
/lab\_host="E. coli SOLR"  
/note="Vector: lambda Uni-ZAP XR, excised phagemid;  
Site\_1: EcoRI; Site\_2: XhoI; Plants were grown to seed  
maturity under conditions favoring seed dormancy (L.  
Doherty at K. Walker-Simmons lab, Washington State  
University, Pullman, WA). Embryos were cut from mature  
dormant seed (Doherty). Total RNA was prepared from these  
embryos, polyA was purified, a cDNA library was made, and  
the cDNA clones were in vivo excised to give phagescript  
phagemids in the T7 Close lab at the University of  
California, Riverside (Chin, Fenton). Plasmid DNA  
preparations and DNA sequencing were performed in the OD  
Anderson lab (all other authors)."

BASE COUNT 145 a 143 c 141 g 157 t  
ORIGIN

Query Match 42.4%; Score 31.8; DB 14; Length 586;  
Best Local Similarity 71.2%; Pred. No. 1.7e+03;  
Matches 42; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 16 TTTTATTTTTTTTGGAAATATAAGCGCGCCCATGGCGCGCCGCAACGCGG 74  
|||||  
Db 4 TTTTATTTTTTTTGGAAACGAGAGCGACGCAAGTATGACGCGCGCGG 62  
|||||

RESULT 7  
AW750324  
LOCUS AW750324 261 bp mRNA linear EST 28-APR-2000  
DEFINITION PM1-BT0585-310100-002-d03 BT0585 Homo sapiens cDNA, mRNA sequence.  
ACCESSION AW750324  
VERSION AW750324.1 GI:7665256  
KEYWORDS EST.

SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 261)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the PAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-BT0585-  
310100-002-d03&t3=2000-01-31&t4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 143.  
Location/Qualifiers  
1..261  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="BT0585"  
/dev\_stage="Adult"  
/note="Organ: breast; Vector: puc18; Site\_1: SmaI; Site\_2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No. 196  
716 - Ludwig Institute for Cancer Research) profiles  
into the pUC 18 vector. Reverse transcription of tissue  
RNA and cDNA amplification were performed under low  
stringency conditions."

BASE COUNT 74 a 46 c 57 g 84 t  
ORIGIN

Query Match 42.1%; Score 31.6; DB 10; Length 261;  
Best Local Similarity 65.7%; Pred. No. 3.1e+03;  
Matches 46; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

OY 5 AAAAATTGAATTTTATTTTGGAAATATAAGCGCGCCCATGGCGCGCGG 64  
|||||  
Db 118 AAGAAAGAAATTTTATTTTGGAAATGAAATGCGCCCATATAGGGTTT 177  
|||||

OY 65 CCAACGCGG 74  
|||||  
Db 178 TTTAAGGAG 187

RESULT 8  
BG177217/c  
LOCUS BG177217 962 bp mRNA linear EST 06-FEB-2001  
DEFINITION 602314394F1 NIH-MGC\_85 Homo sapiens cDNA clone IMAGE:4420366 5',  
mRNA sequence.  
ACCESSION BG177217  
VERSION BG177217.1 GI:12683920  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.  
1 (bases 1 to 962)  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL , Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@db-remail.nih.gov  
Tissue Procurement: Louis Staudt, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at:  
<http://image.llnl.gov>  
Plate: LHAM10157 row: k column: 23  
High quality sequence stop: 403.

FEATURES  
source location/Qualifiers  
1..962  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4420366"  
/clone\_1lb="NIH\_MGC\_85"  
/tissue\_type="lymphoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: lymph; Vector: PCMV-SPOrt6; site\_1: NotI; site\_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC library."

BASE COUNT 278 a 227 c 231 g 225 t 1 others

ORIGIN

Query Match 42.1%; Score 31.6; DB 12; Length 962;  
Best Local Similarity 65.7%; Pred. NO. 1.3e+03;  
Matches 46; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Oy 5 AAAAATTGAATTTATTTTTTTTTTGGAATATAAGCGGCCGACATGGCCCGCGC 64  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 397 AGAAATGGAATTTTTTTTTTTTTTTTTTTTAAGGACTTCGCCGCGCAGTGG 338  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy 65 CCAACGGCGG 74  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 337 CTCACGCTG 328

RESULT 9  
B1798613/c 484 bp mRNA linear EST 02-OCT-2001  
LOCUS H112D05 Endosperm library from Oryza sativa (10 days after anthesis)

DEFINITION ) Oryza sativa cDNA clone H112D05, mRNA sequence.

ACCESSION B1798613

VERSION B1798613.1 GI:15850337

KEYWORDS EST.

SOURCE Oryza sativa.  
Oryza sativa.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharitoidae; Oryzaceae; Oryza.  
1 (bases 1 to 484)  
Dong,H.T., Li,D.B., Zhang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu  
,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.  
A Gene Expression Screen in Oryza sativa  
Unpublished (2001)  
Contact: Dong HT  
Laboratory of Functional Genetics  
Bio-technology Institute of Zhejiang University  
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China  
Tel: 0086-571-86892051  
Fax: 0086-571-86961525  
Email: htdong@zjuem.zju.edu.cn  
Seq primer: M13 forward primer.  
Location/Qualifiers  
1..484  
/organism="Oryza sativa"  
/db\_xref="taxon:4530"  
/clone="H112D05"  
/clone\_1lb="Endosperm library from Oryza sativa (10 days

FEATURES  
source

QY	DB	Match	Similarity	Conservative	Score	DB	Length	Indels	Gaps	Others
16	480	TTTTATTTTTTTTTTTTGGATATATAACGGCCGCCGATGCGCCGCCAGCGCGGA 75	41.6%	42	70.0%	31.2	484	18	0	0
<p>after anthesis")            /tissue_type="Endosperm"            /dev_stage="10 days after anthesis"            /note="Vector: pSPORT2"</p>										
<p>Query Match            Best Local Similarity 70.0%; Pred. No. 2.4e+03;            Matches 42; Conservative 0; Mismatches 18; Indels 0; Gaps 0;</p>										
10	4	TTGAAATTTATTTTTTTTTTTGGATATATAACGGCCGCCGATGCGCCGCCAGCG 69	41.6%	42	70.0%	31.2	501	18	0	0
<p>Query Match            Best Local Similarity 70.0%; Pred. No. 2.4e+03;            Matches 42; Conservative 0; Mismatches 18; Indels 0; Gaps 0;</p>										
<p>RESULT 11            Z305110/c</p>										

LOCUS	AZ305110	581 bp	DNA	linear	GSS-29-SEP-2000
DEFINITION	IM0005P05R Mouse 10kb plasmid U06C1M library	Mus musculus genomic			
ACCESSION	AZ305110				
VERSION	AZ305110.1	GI:10341800			
KEYWORDS	GSS.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 581)				
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Department of Human Genetics Room 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0005 row: P column: 05 Seq primer: CACACAGCAACACCATGACC Class: plasmid ends High quality sequence stop: 581. Location/Qualifiers 1. 581 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="U06C1M0005P05" /clone_id="Mouse 10kb plasmid U06C1M library" /sex="male" /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1147321141gb/AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."				
BASE COUNT	169 a	139 c	153 g	120 t	
ORIGIN					
Query Match	41.3%	Score 31;	DB 17;	Length 581;	
Best Local Similarity	78.7%;	Pred. NO. 2.4e+03;			
Matches 37/	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;	
10 TTGAAATTTTATTTTTTTTTTTTGGATATTAAGCGCGCCCATGCG 56					
Db 341 TTGAATTTTTTTTTTTTCTTTTGGAAATATCCAGTGGCGGTAAAGC 295					
RESULT 12					
12989344					

LOCUS	602 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	2M027208R Mouse 10kb plasmid U06C2M library Mus musculus genomic			
ACCESSION	U06C2M027208 R, DNA sequence.			
VERSION	A2989344			
KEYWORDS	A2989344.1 GI:13860571			
SOURCE	GSS.			
ORGANISM	house mouse.			
REFERENCE	Mus musculus			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.			
	1 (bases 1 to 602)			
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duvall,B., Hamill,C.,			
	Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly			
	,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.			
	and Wright,D., Weiss,R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb			
JOURNAL	plasmid inserts			
COMMENT	Unpublished (2000)			
	Contact: Robert B. Weiss			
	University of Utah			
	University of Utah			
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT			
	84112, USA			
	Tel: 801 585 5606			
	Fax: 801 585 7177			
	Email: ddunn@genetics.utah.edu			
	Insert Length: 10000 Std Error: 0.00			
	Plate: 0272 row: J column: 08			
	Seq primer: CACACAGGAAACAGCTATGACC			
FEATURES	Class: plasmid ends			
SOURCE	High quality sequence stop: 602.			
	Location/Qualifiers			
	1..602			
	/organism="Mus musculus"			
	/strain="C57BL/6J"			
	/db_xref="taxon:10090"			
	/clone="U06C2M027208"			
	/clone_lib="Mouse 10kb plasmid U06C2M library"			
	/sex="Female"			
	/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"			
	/note="Vector: PMD42nv; Purified genomic DNA from M.			
	musculus C57BL/6J (female) was obtained from the Jackson			
	Laboratory Mouse DNA Resource			
	(http://www.jax.org/resources/documents/dnares/). The DNA			
	was hydrodynamically sheared by repeated passage through a			
	0.005 inch orifice at constant velocity. The sheared DNA			
	was blunt end-repaired with T4 DNA polymerase and T4			
	polynucleotide kinase. Adaptor oligonucleotides were			
	ligated to the blunt ends in high molar excess. The			
	adapted DNA was purified and size-selected for a 9.5 to			
	10.5 kb range using preparative agarose gel			
	electrophoresis. Vector DNA was prepared from a derivative			
	of pMD42 (g11473211419b1AR129072.1), a copy-number			
	inducible derivative of plasmid R1. The vector was ligated			
	with adaptors complementary to the insert adaptors and			
	purified. The sheared, adaptor mouse DNA was annealed to			
	adapted vector DNA, and transformed into			
	chemically-competent E. coli XL10-Gold (Stratagene) cells			
	and selected for ampicillin resistance."			
BASE COUNT	136 a	147 c	121 g	198 t
ORIGIN				
Query Match	41.3%	Score 31;	DB 17;	Length 602;
Best Local Similarity	78.7%	Pred. No. 2.3e+03;		
Matches 37; Conservative	0;	Mismatches 10;	Indels	0; Gaps 0;
OY	10	TTGAATTTTAAATTTTTTTTTTTTGAATATTAAGCGCCGCATAGG	56	
DB	120	TTGAATTTTTCCTTTTTCGAAATATCAGTGGCGGCTAAAGG	166	
RESULT 13				
BP916182				



LOCUS BF916182 371 bp mRNA linear EST 18-JAN-2001  
 DEFINITION RCL-UT0083-091200-023-b06 UT0083 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BF916182  
 VERSION BF916182.1 GI:12307640  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCES  
 1 (bases 1 to 371)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,M.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunsehl,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 JOURNAL MEDLINE  
 COMMENT  
 Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-UT0083-091200-023-b06&t3=2000-12-09&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 17  
 High quality sequence stop: 310.  
 Location/Qualifiers  
 1. 371  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="UT0083"  
 /dev\_stage="Adult"  
 /note="Organ: uterus\_tumor; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No.196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."  
 BASE COUNT 76 a 102 c 80 g 113 t  
 ORIGIN  
 Query Match 41.1%; Score 30.8; DB 12; Length 371;  
 Best Local Similarity 63.5%; Pred. No. 3.5e+03;  
 Matches 47; Conservative 0; Mismatches 27; Indels 0; Gaps 0;  
 QY 1 GGCCAAATTTGAATTTATTTTGTGGAATATAAGCGCGCCGATGGCCCG 60  
 Db 275 GGCTCTCATATTTTGTGGAATATAAGCGCGCCGATGGCCCGCA 334  
 QY 61 GCCGCCAAGCGCG 74  
 Db 335 GCGGGAAGCGCAGC 348  
 RESULT 14  
 CNS00YWS 1101 bp DNA linear GSS 26-JUL-1999  
 LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC  
 DEFINITION BACN01A18 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
 ACCESSION AL096911  
 VERSION AL096911.1 GI:5608522  
 KEYWORDS GSS.

SOURCE Drosophila melanogaster.  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 1101)  
 Genoscope.  
 Direct Submision  
 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
 Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.edl.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelBAC11.  
 FEATURES  
 Location/Qualifiers  
 1. 1101  
 /organism="Drosophila melanogaster"  
 /db\_xref="taxon:7227"  
 /clone\_lib="BACN01A18"  
 /clone\_lib="DrosBAC"  
 /plasmid="pBelBAC11"  
 /note="end : 17"  
 BASE COUNT 270 a 179 c 175 g 330 t 147 others  
 ORIGIN  
 Query Match 40.8%; Score 30.6; DB 17; Length 1101;  
 Best Local Similarity 49.2%; Pred. No. 1.9e+03;  
 Matches 32; Conservative 17; Mismatches 16; Indels 0; Gaps 0;  
 QY 2 GGCCAAATTTGAATTTATTTTGTGGAATATAAGCGCGCCGATGGCCCG 61  
 Db 1000 SCCAAMAATTWAMAMTTTTTTTTTTTGTGAGDGVVSVACCCCGCCGCGG 941  
 QY 62 CCGCC 66  
 Db 940 TTGMC 936  
 RESULT 15  
 BM054767 381 bp mRNA linear EST 12-MAR-2002  
 LOCUS le84h05.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens  
 DEFINITION cDNA clone IMAGE:5673825 3', mRNA sequence.  
 ACCESSION BM054767  
 VERSION BM054767.1 GI:16812115  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 381)  
 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scaerice,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Page,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarisvill,R., Williams,T., Jackson,Y. and Bowers,Y.  
 Endocrine Pancreas Consortium  
 Unpublished (2000)  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biohp.harvard.edu  
 Library was constructed by Dr. Douglas Melton DNA sequencing by:





PA (UYRP ) UNIV ROCHESTER.  
 XX  
 PI Zauderer M;  
 XX  
 DR WPI: 2000-376533/32.  
 XX  
 PT Novel method of identifying target epitopes or antigens specific for  
 PT human tumors, cancers and infected cells involving screening expression  
 PT library products of a cell expressing the target epitope -  
 XX  
 PS Disclosure: Fig 1: 132pp; English.  
 XX  
 CC The present sequence represents a fragment of the plasmid p7.5tk,  
 CC comprising the E/L promoter and the beginning of the thymidine kinase  
 CC gene. The pE/Ltk plasmid was used in the course of the invention. The  
 CC specification describes a method for identifying a target epitope.  
 CC The method comprises screening the products of an expression library  
 CC from a cell expressing the target epitope with cytotoxic T cells  
 CC generated against the cell to identify DNA clones expressing the target  
 CC epitope. The method may also comprise providing a cytotoxic T cell  
 CC specific for a gene product differentially expressed by a cell and  
 CC measuring the cross-reactivity of the cytotoxic T cell. The methods are  
 CC useful for identifying tumour specific target epitopes and antigens which  
 CC are useful in immunogenic compositions or vaccines to induce the  
 CC regression of tumors, cancers or infections in mammals. The genes  
 CC expressed in a panel of tumour cells that are derived from single  
 CC immortalised, non-tumourigenic cell line are used to generate HLA  
 CC restricted cytotoxic T cells which are evaluated for activity against  
 CC tumour cells. The method is useful to identify potential antigens  
 CC expressed not only by the pathogen but also by the host cells whose gene  
 CC expression is altered as a result of infection. The differential gene  
 CC expression strategies can be applied to identify immunogenic molecules  
 CC of cells infected with virus, fungus or mycobacterium.  
 XX  
 SQ Sequence 75 BP; 19 A; 16 C; 19 G; 21 T; 0 other;

Query Match 100.0%; Score 75; DB 21; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-12;  
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGCCTAAATGAAATTTATTTTGGAAATATAAGCGCGCCATGGGCCCG 60  
 |||||||  
 Db 1 GGCCTAAATGAAATTTATTTTGGAAATATAAGCGCGCCATGGGCCCG 60  
 |||||||

OY 61 GCCGCCAACGGCGGA 75  
 |||||||  
 Db 61 GCCGCCAACGGCGGA 75  
 |||||||

RESULT 2  
 ABA01475  
 ID ABA01475 standard; DNA; 75 BP.  
 XX  
 AC ABA01475;  
 XX  
 DT 04-FEB-2002 (first entry)  
 XX  
 DE Partial pE/Ltk sequence.  
 XX  
 KW Cell death; toxic gene; tumour suppressor; ds.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200172995-A2.  
 PD 04-OCT-2001.  
 XX  
 PF 28-MAR-2001; 2001WO-US09953.  
 XX  
 PR 28-MAR-2000; 2000US-0192586.  
 PR 10-MAY-2000; 2000US-020343.  
 PR 23-JAN-2001; 2001US-0263226.  
 PR 27-FEB-2001; 2001US-0271426.

XX  
 PA (UYRP ) UNIV ROCHESTER.  
 XX  
 PI Zauderer M, Smith ES;  
 XX  
 DR WPI: 2001-570897/64.  
 XX  
 PT Selecting target polynucleotides, particularly toxic genes, involves  
 PT introducing a library of insert polynucleotides into a host cell  
 PT population, where the target polynucleotide promotes cell death -  
 XX  
 PS Disclosure: Fig 1: 359pp; English.  
 XX  
 CC The present invention relates to a method for selecting a target  
 CC polynucleotide. The method comprises introducing into a host cell  
 CC population a library of insert polynucleotides, where expression of the  
 CC target polynucleotide directly or indirectly promotes host cell death.  
 CC The cells are cultured and the insert polynucleotides are collected from  
 CC the cells which die. The method is useful for selecting target  
 CC polynucleotides, particularly polynucleotides which alter cell phenotypes  
 CC of induce or inhibit cell death. The method can be used to isolate toxic  
 CC genes such as tumour suppressors. The present sequence was used to  
 CC illustrate the method of the present invention.  
 XX  
 SQ Sequence 75 BP; 19 A; 16 C; 19 G; 21 T; 0 other;

Query Match 100.0%; Score 75; DB 22; Length 75;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-12;  
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGCCTAAATGAAATTTATTTTGGAAATATAAGCGCGCCATGGGCCCG 60  
 |||||||  
 Db 1 GGCCTAAATGAAATTTATTTTGGAAATATAAGCGCGCCATGGGCCCG 60  
 |||||||

OY 61 GCCGCCAACGGCGGA 75  
 |||||||  
 Db 61 GCCGCCAACGGCGGA 75  
 |||||||

RESULT 3  
 AAD31776  
 ID AAD31776 standard; DNA; 75 BP.  
 XX  
 AC AAD31776;  
 XX  
 DT 18-JUN-2002 (first entry)  
 XX  
 DE pE/Ltk vector comprising E/L promoter and vaccinia virus tk DNA.  
 XX  
 KW Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;  
 KW vaccine; immune response; cytostatic; pE/Ltk vector; thymidine kinase;  
 KW ds.  
 XX  
 OS Vaccinia virus.  
 XX  
 OS Synthetic.  
 XX  
 FH Key  
 FH CDS  
 FT 52..75  
 FT /\*tag= a  
 FT /product= "thymidine kinase protein"  
 XX  
 PN US2002018785-A1.  
 PD 14-FEB-2002.  
 XX  
 PF 02-APR-2001; 2001US-0822250.  
 XX  
 PR 22-SEP-1997; 97US-0935377.  
 XX  
 PA (UYRP ) UNIV ROCHESTER.  
 XX  
 PI Zauderer M;

```
DR WPI: 2002-239252/29.
XX P-PSDB: AAE19944.
XX
XX Representational Difference Analysis method for identification of
PT antigens recognized by cytotoxic T cells and specific for human tumors,
PT comprises improved selection of genes encoding target antigens
XX
XX Example 1; Fig 1; 54pp; English.
XX
XX The present invention relates to novel methods for the identification
CC of antigens recognised by cytotoxic T cells (CTLs) and specific for
CC human tumours, cancers and infected cells. The method involves screening
CC the products of an expression library generated from DNA/RNA of a cell
CC expressing a target epitope with cytotoxic T cells generated against
CC the cell to identify DNA clones expressing target epitope or providing
CC cytotoxic T cells specific for a gene product differentially expressed
CC by a cell and measuring the cross-reactivity of the cytotoxic T cells
CC for cells expressing a target epitope in which the target epitope is
CC identified as a gene product inducing cytotoxic T cells. The method is
CC useful for identifying a target epitope or antigen specific for a tumour
CC cell. The target epitope is also useful for identifying target antigens
CC in other target cells against which it is desirable to induce cell-
CC mediated immunity. The antigen identified by the method is useful
CC in immunogenic compositions and vaccine preparations to induce the
CC regression of tumours, cancers and infections in mammals. The invention
CC also relates to vaccinia viral vectors which are useful for treating
CC tumour-bearing mammals, including humans to generate immune response
CC against the tumour cells. They are also useful for immunising or
CC vaccinating tumour-free subjects to prevent tumour formation. The
CC present sequence is pE/Ltk (thymidine kinase) vector comprising a
CC synthetic early/late (E/L) promoter and vaccinia virus tk DNA fragment.
CC This sequence is used in the exemplification of the invention.
XX
XX Sequence 75 BP: 19 A; 16 C; 19 G; 21 T; 0 other;
SQ
Query Match 100.0%; Score 75; DB 24; Length 75;
Best Local Similarity 100.0%; Pred. No. 1,5e-12;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCAAAATGAAATTTATTTTGGAAATATAAGCGCGCCATGGCCCG 60
XX |
XX |
XX |
DB 1 GGGCAAAATGAAATTTATTTTGGAAATATAAGCGCGCCATGGCCCG 60
QY 61 GCGGCCAACGGCGGA 75
DB 61 GCGGCCAACGGCGGA 75
RESULT 4
ABA01484
ID ABA01484 standard; DNA: 59 BP.
XX
XX ABA01484;
XX
XX 04-FEB-2002 (first entry)
XX
XX PCR primer MM438.
XX
XX PCR primer; cell death; toxic gene; tumour suppressor; ss.
XX
XX Synthetic.
XX
XX WO200172995-A2.
XX
XX 04-OCT-2001.
XX
XX 28-MAR-2001; 2001WO-US09953.
XX
XX 28-MAR-2000; 2000US-0192586.
XX
XX 10-MAY-2000; 2000US-0203343.
XX
XX 23-JAN-2001; 2001US-0263226.
XX
XX 27-FEB-2001; 2001US-0271426.
XX
```

```
PA (UYRP ) UNIV ROCHESTER.
XX
XX Zauderer M, Smith ES;
XX
XX WPI: 2001-570897/64.
XX
XX Selecting target polynucleotides, particularly toxic genes, involves
PT introducing a library of insert polynucleotides into a host cell
PT population, where the target polynucleotide promotes cell death -
XX
XX Example 1; Page 135; 359pp; English.
XX
XX The present invention relates to a method for selecting a target
CC polynucleotide. The method comprises introducing into a host cell
CC population a library of insert polynucleotides, where expression of the
CC target polynucleotide directly or indirectly promotes host cell death.
CC The cells are cultured and the insert polynucleotides are collected from
CC the cells which die. The method is useful for selecting target
CC polynucleotides, particularly polynucleotides which alter cell phenotypes
CC of induce or inhibit cell death. The method can be used to isolate toxic
CC genes such as tumour suppressors. The present sequence is a PCR primer,
CC which was used in an example from the present invention.
XX
XX Sequence 59 BP: 16 A; 10 C; 12 G; 21 T; 0 other;
SQ
Query Match 78.7%; Score 59; DB 22; Length 59;
Best Local Similarity 100.0%; Pred. No. 5,6e-08;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCAAAATGAAATTTATTTTGGAAATATAAGCGCGCCATGGCCCG 59
XX |
XX |
XX |
DB 1 GGGCAAAATGAAATTTATTTTGGAAATATAAGCGCGCCATGGCCCG 59
RESULT 5
ABA01485/c
ID ABA01485 standard; DNA: 59 BP.
XX
XX ABA01485;
XX
XX 04-FEB-2002 (first entry)
XX
XX PCR primer MM439.
XX
XX PCR primer; cell death; toxic gene; tumour suppressor; ss.
XX
XX Synthetic.
XX
XX WO200172995-A2.
XX
XX 04-OCT-2001.
XX
XX 28-MAR-2001; 2001WO-US09953.
XX
XX 28-MAR-2000; 2000US-0192586.
XX
XX 10-MAY-2000; 2000US-0203343.
XX
XX 23-JAN-2001; 2001US-0263226.
XX
XX 27-FEB-2001; 2001US-0271426.
XX
XX (UYRP ) UNIV ROCHESTER.
XX
XX Zauderer M, Smith ES;
XX
XX WPI: 2001-570897/64.
XX
XX Selecting target polynucleotides, particularly toxic genes, involves
PT introducing a library of insert polynucleotides into a host cell
PT population, where the target polynucleotide promotes cell death -
XX
XX Example 1; Page 135; 359pp; English.
XX
XX The present invention relates to a method for selecting a target
CC polynucleotide. The method comprises introducing into a host cell
```

CC population a library of insert polynucleotides, where expression of the  
CC target polynucleotide directly or indirectly promotes host cell death.  
CC The cells are cultured and the insert polynucleotides are collected from  
CC the cells which die. The method is useful for selecting target  
CC polynucleotides, particularly polynucleotides which alter cell phenotypes  
CC of induce or inhibit cell death. The method can be used to isolate toxic  
CC genes such as tumour suppressors. The present sequence is a PCR primer,  
CC which was used in an example from the present invention.

XX  
SQ Sequence 59 BP; 21 A; 12 C; 10 G; 16 T; 0 other;

Query Match 78.7%; Score 59; DB 22; Length 59;  
Best Local Similarity 100.0%; Pred. No. 5.6e-08;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 AAAAAATTGAATTTATTTTGTGGAATATATAAGCGCGCCCATGGCGCC 63  
DB 59 AAAAAATTGAATTTATTTTGTGGAATATATAAGCGCGCCCATGGCGCC 1

RESULT 6  
AAD31796  
ID AAD31796 standard; DNA; 59 BP.  
AC AAD31796;  
XX 18-JUN-2002 (first entry)  
DE MM438 oligonucleotide used to construct pE/Ltk plasmid.  
XX Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;  
XX vaccine; immune response; cytostatic; pE/Ltk plasmid; thymidine kinase;  
XX ds.  
XX Unidentified.  
XX US2002018785-A1.  
XX 14-FEB-2002.  
XX 02-APR-2001; 2001US-0822250.  
XX 22-SEP-1997; 97US-0935377.  
XX (UYRP ) UNIV ROCHESTER.  
PA Zauderer M;  
PI WPI; 2002-239252/29.  
DR Representational Difference Analysis method for identification of  
PT antigens recognized by cytotoxic T cells and specific for human tumors,  
PT comprises improved selection of genes encoding target antigens -  
XX  
XX  
PS Example 9; Page 23; 54pp; English.

XX The present invention relates to novel methods for the identification  
CC of antigens recognised by cytotoxic T cells (CTLs) and specific for  
CC human tumours, cancers and infected cells. The method involves screening  
CC the products of an expression library generated from DNA/RNA of a cell  
CC expressing a target epitope with cytotoxic T cells generated against  
CC the cell to identify DNA clones expressing target epitope or providing  
CC cytotoxic T cells specific for a gene product differentially expressed  
CC by a cell and measuring the cross-reactivity of the cytotoxic T cells  
CC for cells expressing a target epitope in which the target epitope is  
CC identified as a gene product inducing cytotoxic T cells. The method is  
CC useful for identifying a target epitope or antigen specific for a tumour  
CC cell. The target epitope is also useful for identifying target antigens  
CC in other target cells against which it is desirable to induce cell-  
CC mediated immunity. The antigen identified by the method is useful  
CC in immunogenic compositions and vaccine preparations to induce the  
CC regression of tumours, cancers and infections in mammals. The invention  
CC also relates to vaccinia viral vectors which are useful for treating

CC tumour-bearing mammals, including humans to generate immune response  
CC against the tumour cells. They are also useful for immunising or  
CC vaccinating tumour-free subjects to prevent tumour formation. The  
CC present DNA sequence is an oligonucleotide which is used to construct  
CC pE/Ltk (thymidine kinase) plasmid comprising a synthetic early/late  
CC (E/L) promoter and vaccinia virus tk DNA fragment. This oligo is used  
CC in the exemplification of the invention.

XX  
SQ Sequence 59 BP; 16 A; 10 C; 12 G; 21 T; 0 other;

Query Match 78.7%; Score 59; DB 24; Length 59;  
Best Local Similarity 100.0%; Pred. No. 5.6e-08;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGCAAAATTTGAATTTATTTTGTGGAATATATAAGCGCGCCCATGGCGCC 59  
DB 1 GCGCAAAATTTGAATTTATTTTGTGGAATATATAAGCGCGCCCATGGCGCC 59

RESULT 7  
AAD31797/C  
ID AAD31797 standard; DNA; 59 BP.  
AC AAD31797;  
XX 18-JUN-2002 (first entry)  
DE MM439 oligonucleotide used to construct pE/Ltk plasmid.  
XX Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;  
XX vaccine; immune response; cytostatic; pE/Ltk plasmid; thymidine kinase;  
XX ds.  
XX Unidentified.  
XX US2002018785-A1.  
XX 14-FEB-2002.  
XX 02-APR-2001; 2001US-0822250.  
XX 22-SEP-1997; 97US-0935377.  
XX (UYRP ) UNIV ROCHESTER.  
PA Zauderer M;  
PI WPI; 2002-239252/29.  
DR Representational Difference Analysis method for identification of  
PT antigens recognized by cytotoxic T cells and specific for human tumors,  
PT comprises improved selection of genes encoding target antigens -  
XX  
XX  
PS Example 9; Page 23; 54pp; English.

XX The present invention relates to novel methods for the identification  
CC of antigens recognised by cytotoxic T cells (CTLs) and specific for  
CC human tumours, cancers and infected cells. The method involves screening  
CC the products of an expression library generated from DNA/RNA of a cell  
CC expressing a target epitope with cytotoxic T cells generated against  
CC the cell to identify DNA clones expressing target epitope or providing  
CC cytotoxic T cells specific for a gene product differentially expressed  
CC by a cell and measuring the cross-reactivity of the cytotoxic T cells  
CC for cells expressing a target epitope in which the target epitope is  
CC identified as a gene product inducing cytotoxic T cells. The method is  
CC useful for identifying a target epitope or antigen specific for a tumour  
CC cell. The target epitope is also useful for identifying target antigens  
CC in other target cells against which it is desirable to induce cell-  
CC mediated immunity. The antigen identified by the method is useful  
CC in immunogenic compositions and vaccine preparations to induce the  
CC regression of tumours, cancers and infections in mammals. The invention  
CC also relates to vaccinia viral vectors which are useful for treating  
CC tumour-bearing mammals, including humans to generate immune response

CC against the tumour cells. They are also useful for immunising or  
CC vaccinating tumour-free subjects to prevent tumour formation. The  
CC present DNA sequence is an oligonucleotide which is used to construct  
CC pE/Ltk (thymidine kinase) plasmid comprising a synthetic early/late  
CC (E/L) promoter and vaccinia virus tk DNA fragment. This oligo is used  
CC in the exemplification of the invention.

XX Sequence 59 BP; 21 A; 12 C; 10 G; 16 T; 0 other;

SO Query Match 78.7%; Score 59; DB 24; Length 59;  
Best Local Similarity 100.0%; Pred. No. 5.6e-08;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 AAAAAATGAAATTTATTTTGGAAATATAAGCGCGCCATGCGCCGCC 63  
DB 59 AAAAAATGAAATTTATTTTGGAAATATAAGCGCGCCATGCGCCGCC 1

RESULT 8  
ABA01491  
ID ABA01491 standard; DNA; 77 BP.

XX ABA01491;

XX 04-FEB-2002 (first entry)

DE PCR primer E10va.

XX PCR primer; cell death; toxic gene; tumour suppressor; ss.

XX Synthetic.

XX WO200172995-A2.

XX 04-OCT-2001.

XX 28-MAR-2001; 2001WO-US09953.

XX 28-MAR-2000; 2000US-0192586.

XX 10-MAY-2000; 2000US-0203343.

XX 23-JAN-2001; 2001US-0263226.

XX 27-FEB-2001; 2001US-02711426.

XX (UYRP ) UNIV ROCHESTER.

XX Zauderer M, Smith ES;

XX WPI; 2001-570897/64.

XX Example 1; Page 136; 359pp; English.

CC The present invention relates to a method for selecting a target  
CC polynucleotide. The method comprises introducing into a host cell  
CC a population a library of insert polynucleotides, where expression of the  
CC target polynucleotide directly or indirectly promotes host cell death.  
CC The cells are cultured and the insert polynucleotides are collected from  
CC the cells which die. The method is useful for selecting target  
CC polynucleotides, particularly polynucleotides which alter cell phenotypes  
CC of induce or inhibit cell death. The method can be used to isolate toxic  
CC genes such as tumour suppressors. The present sequence is a PCR primer,  
CC which was used in an example from the present invention.

XX Sequence 77 BP; 29 A; 7 C; 11 G; 30 T; 0 other;

SO Query Match 56.5%; Score 42.4; DB 22; Length 77;  
Best Local Similarity 97.7%; Pred. No. 0.0033;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGCCAAAATGAAATTTATTTTGGAAATATAAGC 44

DB 1 GGCCAAAATGAAATTTATTTTGGAAATATAAGC 44

RESULT 9  
AAD31803

ID AAD31803 standard; DNA; 77 BP.

XX AAD31803;

XX 18-JUN-2002 (first entry)

DE E10va oligonucleotide used to construct pE/Ltk-ova plasmid.

XX Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;

XX Immune response; cytostatic; pE/Ltk-ova plasmid; thymidine kinase;

XX vaccine; ovalbumin; ds.

XX Unidentified.

XX US2002018785-A1.

XX 14-FEB-2002.

XX 02-APR-2001; 2001US-0822250.

XX 22-SEP-1997; 97US-0935377.

XX (UYRP ) UNIV ROCHESTER.

XX Zauderer M;

XX WPI; 2002-239252/29.

XX Example 9; Page 23; 54pp; English.

CC The present invention relates to novel methods for the identification  
CC of antigens recognised by cytotoxic T cells (CTLs) and specific for  
CC human tumours, cancers and infected cells. The method involves screening  
CC the products of an expression library generated from DNA/RNA of a cell  
CC expressing a target epitope with cytotoxic T cells generated against  
CC the cell to identify DNA clones expressing target epitope or providing  
CC cytotoxic T cells specific for a gene product differentially expressed  
CC by a cell and measuring the cross-reactivity of the cytotoxic T cells  
CC for cells expressing a target epitope in which the target epitope is  
CC identified as a gene product inducing cytotoxic T cells. The method is  
CC useful for identifying a target epitope or antigen specific for a tumour  
CC cell. The target epitope is also useful for identifying target antigens  
CC in other target cells against which it is desirable to induce cell-  
CC mediated immunity. The antigen identified by the method is useful  
CC in immunogenic compositions and vaccine preparations to induce the  
CC regression of tumours, cancers and infections in mammals. The invention  
CC also relates to vaccinia viral vectors which are useful for treating  
CC tumour-bearing mammals, including humans to generate immune response  
CC against the tumour cells. They are also useful for immunising or  
CC vaccinating tumour-free subjects to prevent tumour formation. The  
CC present DNA sequence is an oligonucleotide which is used to construct  
CC pE/Ltk (thymidine kinase)-ova plasmid comprising a synthetic E/L  
CC (early/late) promoter, tk DNA fragment and a DNA encoding cytotoxic  
CC T-cell epitope for ovalbumin. This oligo is used in the exemplification  
CC of the invention.

XX Sequence 77 BP; 29 A; 7 C; 11 G; 30 T; 0 other;

SO Query Match 56.5%; Score 42.4; DB 24; Length 77;  
Best Local Similarity 97.7%; Pred. No. 0.0033;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GGCCAAAATGAAATTTATTTTGGAAATATAAGC 44





```

RESULT 12 '
AAZ46843/C
ID AAZ46843 standard; DNA; 78 BP.
XX
XX AAZ46843;
XX
XX 10-APR-2000 (first entry)
XX
XX Myxoma virus early/late promoter fragment generating oligo.
XX
XX Myxoma virus; CNCM I-1990; vaccine; myxomatosis; hemorrhagic disease;
XX rabbit; immunisation; promoter; ss.
XX
XX Myxoma virus.
XX
XX EP972840-A2.
XX
XX 19-JAN-2000.
XX
XX 10-JUN-1999; 99EP-0500099.
XX
XX 10-JUN-1998; 98ES-0001219.
XX
XX (PARA-) FUNDACION PARA EL ESTUDIO Y DEFENSA NATU.
XX (NAIN-) INST NACIONAL INVESTIGACION & TECNOLOGIA.
XX
XX Barcena DR, Blasco Lozano R, Morales Camarazana M, Pages Mante A;
XX Parra Fernandez F, Sanchez Vizcaino JM, Torres Trillo JM;
XX Vazquez Ruiz B;
XX
XX WPI; 2000-108130/10.
XX
XX Novel recombinant virus, used to treat myxomatosis and rabbit
XX hemorrhagic disease, in wild rabbits -
XX
XX Disclosure; Page 5; 29pp; English.
XX
XX The invention provides a recombinant myxoma virus deposited as
XX CNCM I-1990. The recombinant virus is used as a combined vaccine against
XX both myxomatosis and rabbit hemorrhagic disease, in wild rabbits. The
XX combined vaccine has a controlled self-propagating capacity which means
XX that not every animal needs to be individually immunized to get
XX efficient employment of the vaccine in wild rabbit populations. Sequences
XX AAZ46843-44 represent oligos for generating a myxoma virus early/late
XX promoter fragment.
XX
XX Sequence 78 BP; 30 A; 13 C; 9 G; 26 T; 0 other;
XX
XX Query Match 53.1%; Score 39.8; DB 21; Length 78;
XX Best Local Similarity 86.3%; Pred. No. 0.018; 7; Indels 0; Gaps 0;
XX Matches 44; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
XX 5 AAAAAATGAAATTTATTTTGGAAATTAAGCGCCGCATG 55
XX ||||||||||||||||||||||||||||| |||||
XX 54 AAAAAATGAAATTTATTTTGGAAATTAATAATACGAGATG 4
XX
XX RESULT 13
XX AAQ40300/C
XX ID AAQ40300 standard; DNA; 6474 BP.
XX
XX AAQ40300;
XX
XX 02-AUG-1993 (first entry)
XX
XX Sequence of plasmid pself-gp160MN.
XX
XX Plasmid; cloning; restriction site; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH misc_feature 1..55

```

```

FT FT /tag- a
FT FT /label= pTZ19R
FT FT misc_feature
FT FT complement (56..108)
FT FT /tag- b
FT FT /label= linker I in rc orientation
FT FT CDS
FT FT complement (110..860)
FT FT /tag- c
FT FT /label= E. coli gpt
FT FT promoter
FT FT complement (861..1245)
FT FT /tag- d
FT FT /label= Vaccinia virus p7.5
FT FT /note = "starting with the p7.5 internal NdeI site
FT FT at posn. 1241"
FT FT 1339..1344
FT FT /tag- e
FT FT /label= HpaI site
FT FT misc_feature
FT FT complement (1259..3916)
FT FT /tag- f
FT FT /label= HIV-MN env gene
FT FT promoter
FT FT complement (3917..3970)
FT FT /tag- g
FT FT /label= vaccinia virus synthetic early/late
FT FT promoter
FT FT misc_feature
FT FT complement (3971..4015)
FT FT /tag- h
FT FT /label= linker II
FT FT misc_feature
FT FT complement (4016..6474)
FT FT /tag- i
FT FT /label= pTZ19R
XX
XX AU9221269-A.
XX
XX 04-MAR-1993.
XX
XX 25-AUG-1992; 92AU-0021269.
XX
XX 26-AUG-1991; 91US-0750080.
XX PR 20-JUL-1992; 92US-0914738.
XX
XX (IMMO ) IMMUNO AG.
XX
XX Dörner F, Falkner FG, Pfeleiderer M, Schefflinger F;
XX WPI; 1993-126461/16.
XX
XX Modified eukaryotic cytoplasmic DNA virus prodn. - involves
XX PT direct molecular cloning of modified DNA molecule contg.
XX PT cytoplasmic DNA virus genome
XX
XX PS Example; Pages 169-172; 206pp; English.
XX
XX The synthetic early/late promoter self was used to express the
XX gp160-gene of the HIV-1 MN strain. For the construction of pL2
XX CC the 0.6kb XbaI-ClaI fragment of the plasmid pTM3 was substituted
XX CC by an XbaI-ClaI adaptor fragment consisting of the annealed
XX CC oligonucleotide 0-542 and 0-544. The intermediate plasmid
XX CC resulting from this cloning step was called pL1. The 0.94kb
XX CC AatII-SphI fragment were substituted by the AatII-SphI adaptor
XX CC fragment consisting of the annealed oligonucleotide 0-541 and
XX CC 0-543. The resulting plasmid was called pL2. The XbaI-SphI
XX CC fragment was treated with Klenow-polymerase and inserted between
XX CC the PvuII sites of the plasmid pTZ19R. The resulting plasmid was
XX CC called pTZ-L2. The 0.6kb ClaI-NcoI fragment (the T7-promoter-EKC-
XX CC sequence) was replaced with a synthetic promoter fragment
XX CC consisting of the annealed oligonucleotide 0-selfI and 0-selfPI.
XX CC The 239bp Sall-NdeI fragment of the resulting intermediate plasmid
XX CC was substituted by the Sall-NdeI adaptor consisting of the annealed
XX CC oligonucleotides 0-830 and 0-857. The resulting plasmid was called
XX CC pself-gpt-L2. The 3.1kb env gene containing the EcoRI-PvuII
XX CC fragment of pMNEV1 was inserted into the EcoRI and StuI cut plasmid
XX CC pself-gpt-L2 resulting in the intermediate plasmid pself-gp160.1.
XX CC The 0.8kb NcoI-NsiI fragment of pself-gp160 was substituted by a
XX CC PCR-generated 0.31kb NcoI-NsiI fragment resulting in the final

```

CC plasmid pself-gp160MN. The primers used for the PCR reaction were  
 CC o-NCOI and o-NSII.  
 XX  
 SQ Sequence 6474 BP; 1648 A; 1533 C; 1410 G; 1880 T; 4 other;

Query Match 52.8%; Score 39.6; DB 14; Length 6474;  
 Best Local Similarity 83.3%; Pred. No. 0.048;  
 Matches 45; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 5 AAAAATGAAATTTATTTTGGAAATATAAGCGCGCCCATGGGCC 58  
 |||  
 DB 3964 AAAAATGAAATTTATTTTGGAAATATAAGCGCCCATGGGCC 3911

RESULT 14  
 AAA89877/C  
 ID AAA89877 standard; DNA: 6474 BP.

XX AAA89877;

XX 26-JAN-2001 (first entry)

XX Plasmid pself-gp160 MN.

XX Vaccinia; fowlpox; virus; immune response; HIV; gp-160; gag;

KW gag-pol; ds.

XX Synthetic.

XX US6103244-A.

XX 15-AUG-2000.

XX 22-MAY-1996; 96US-0651472.

XX 19-DEC-1994; 94US-0358928.

XX 26-AUG-1991; 91US-0750080.

XX 20-JUL-1992; 92US-0914738.

XX (IMMO ) IMMUNO AG.

XX Pflaenderer M, Falkner FG, Scheifflinger F, Dörner F;

XX WPI; 2000-557665/51.

XX Use of modified vaccinia virus and fowlpox virus for generating or  
 PT priming an immune response against HIV gp160, HIV Gag and HIV Gag-Pol  
 PT proteins -

XX Example 9; Column 147-154; 171pp; English.

XX The present invention relates to the use of modified vaccinia virus and  
 CC fowlpox virus for generating or priming an immune response against a  
 CC heterologous protein in a vertebrate. Suitable proteins include HIV  
 CC proteins such as HIV gp160, HIV Gag and HIV Gag-Pol proteins. The  
 CC present sequence was associated with the generation or use of the  
 CC modified viruses.

XX Sequence 6474 BP; 1649 A; 1533 C; 1411 G; 1881 T; 0 other;

Query Match 52.8%; Score 39.6; DB 21; Length 6474;

Best Local Similarity 83.3%; Pred. No. 0.048;  
 Matches 45; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 5 AAAAATGAAATTTATTTTGGAAATATAAGCGCGCCCATGGGCC 58  
 |||  
 DB 3964 AAAAATGAAATTTATTTTGGAAATATAAGCGCCCATGGGCC 3911

RESULT 15  
 AAS12795/C  
 ID AAS12795 standard; DNA: 6474 BP.  
 XX

AC AAS12795;  
 XX 21-NOV-2001 (first entry)  
 DT  
 XX  
 XX Plasmid pself-gp160MN DNA sequence.

DE Cytoplasmic DNA virus; direct molecular cloning; vaccinia virus; insect;  
 XX unique restriction endonuclease cleavage site; infectious virion; ds;  
 KW helper virus; poxvirus; iridovirus; vertebrate; multiple cloning site.  
 KM  
 XX

OS Synthetic.

XX US6265183-B1.

XX 24-JUL-2001.

XX 19-DEC-1994; 94US-0358928.

XX 26-AUG-1991; 91US-0750080.

XX 20-JUL-1992; 92US-0914738.

XX (BAXT ) BAXTER AG.

XX Dörner F, Scheifflinger F, Falkner FG, Pflaenderer M;

XX WPI; 2001-535006/59.

XX Producing recombinant protein using modified vaccinia viral expression  
 PT system, comprises directly cloning heterologous insert encoding protein  
 PT into the viral genome into unique restriction endonuclease cleavage  
 PT site -

XX Example 9; Column 149-154; 172pp; English.

XX The invention relates to a method for producing a modified eukaryotic  
 CC cytoplasmic DNA virus by direct molecular cloning of a modified DNA  
 CC molecule comprising a modified cytoplasmic DNA virus genome such as a  
 CC vaccinia virus, containing a heterologous insert encoding a protein. The  
 CC method involves molecularly cloning the DNA directly into a host cell via  
 CC a unique restriction endonuclease cleavage site, to be packaged into  
 CC infectious virions and then recovering them. The host cell is infected  
 CC with a helper virus for this purpose. The method is useful for producing  
 CC recombinant proteins and modified eukaryotic cytoplasmic DNA viruses such  
 CC as poxviruses and iridoviruses found in vertebrates and insects. This  
 CC sequence represents a plasmid pself-gp160MN used in the construction of  
 CC chimeric vaccinia viruses.

XX Sequence 6474 BP; 1649 A; 1534 C; 1410 G; 1881 T; 0 other;

Query Match 52.8%; Score 39.6; DB 22; Length 6474;

Best Local Similarity 83.3%; Pred. No. 0.048;  
 Matches 45; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 5 AAAAATGAAATTTATTTTGGAAATATAAGCGCGCCCATGGGCC 58  
 |||  
 DB 3964 AAAAATGAAATTTATTTTGGAAATATAAGCGCCCATGGGCC 3911

Search completed: November 10, 2002, 05:58:25  
 Job time : 90.4933 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:58:40 ; Search time 18.6657 Seconds  
(without alignments)  
1425.554 Million cell updates/sec

Title: US-08-935-377-3

Perfect score: 75  
Sequence: 1 GGCCAAAATGAAATTTTA.....GCCCGGCCCAACGCGGA 75

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 320260 seqs, 177392727 residues

Total number of hits satisfying chosen parameters: 640520

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications\_NA:\*

- 1: /cgn2\_6/ptodata/1/pubna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubna/PC1\_NEM\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubna/US06\_NEM\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubna/US07\_NEM\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubna/PCRTS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubna/US08\_NEM\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubna/US09\_NEM\_PUB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubna/US09\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubna/US10\_NEM\_PUB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubna/US10\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubna/US60\_NEM\_PUB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	75	10	US-09-822-250-3
2	75	100.0	75	10	US-09-987-456-142
3	59	78.7	59	10	US-09-822-250-75
4	59	78.7	59	10	US-09-822-250-26
5	42.4	56.5	77	10	US-09-822-250-32
6	38.4	51.2	77	10	US-09-822-250-33
7	37	49.3	69	10	US-09-822-250-1
8	37	49.3	69	10	US-09-987-456-140
9	29.6	39.5	62944	10	US-09-954-456-2257
10	28	37.3	27483	10	US-09-764-877-2928
11	27.8	37.1	6855	10	US-09-764-864-1694
12	27.8	37.1	21045	10	US-09-764-864-1695
13	27.2	36.3	17784	10	US-09-764-877-3158
14	26.8	35.7	338	10	US-09-867-701-8272
15	26.8	35.7	468	10	US-09-969-373-257
16	26.8	35.7	584	12	US-10-001-879-21
17	26.8	35.7	1215	9	US-09-938-842A-1206
18	26.8	35.7	1905	9	US-09-938-842A-5193
19	26.8	35.7	3690	12	US-10-052-586-517

20	26.4	35.2	453	10	US-09-922-217-1047	Sequence 1047, Ap
21	26.4	35.2	453	10	US-09-833-263-1047	Sequence 1047, Ap
22	26.4	35.2	1172	10	US-09-764-869-1651	Sequence 1651, Ap
23	26.4	35.2	1172	10	US-09-764-869-1653	Sequence 1653, Ap
24	26.4	35.2	2000	9	US-09-938-842A-3467	Sequence 3467, Ap
25	26.2	34.9	31314	10	US-09-764-877-3875	Sequence 3875, Ap
26	26	34.7	2136	10	US-09-750-703-5	Sequence 5, Appl
27	26	34.7	84539	10	US-09-962-703-36	Sequence 36, Appl
28	25.8	34.4	240	10	US-09-878-574-7281	Sequence 7281, Ap
29	25.8	34.4	250	10	US-09-878-574-7255	Sequence 7255, Ap
30	25.8	34.4	553	10	US-09-864-761-13017	Sequence 13017, A
31	25.8	34.4	46718	10	US-09-816-093-3	Sequence 3, Appl1
32	25.6	34.1	95	10	US-09-864-761-18342	Sequence 18342, A
33	25.6	34.1	167	10	US-09-864-761-31398	Sequence 31398, A
34	25.6	34.1	355	10	US-09-960-352-14757	Sequence 14757, A
35	25.6	34.1	520	10	US-09-864-761-1584	Sequence 1584, Ap
36	25.6	34.1	470	10	US-09-864-761-14871	Sequence 14871, A
37	25.6	34.1	865	10	US-09-925-300-301	Sequence 301, App
38	25.4	33.9	180	10	US-09-815-343-734	Sequence 734, App
39	25.4	33.9	500	10	US-09-764-847-388	Sequence 388, App
40	25.4	33.9	4599	9	US-09-974-298-167	Sequence 167, App
41	25.4	33.9	32191	10	US-09-764-869-1955	Sequence 1955, Ap
42	25.2	33.6	425	10	US-09-834-975-451	Sequence 451, App
43	25.2	33.6	480	9	US-10-046-935-51	Sequence 51, Appl
44	25.2	33.6	2000	9	US-09-938-842A-3811	Sequence 3811, Ap
45	25.2	33.6	2000	10	US-09-887-576-135	Sequence 135, App

#### ALIGNMENTS

RESULT 1  
US-09-822-250-3  
Sequence 3, Application US/09822250  
Patent NO. US2002018785A1  
GENERAL INFORMATION:  
APPLICANT: Zanderer, Maurice  
TITLE OR INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus  
FILE REFERENCE: 1821.0010001  
CURRENT APPLICATION NUMBER: US/09/822,250  
CURRENT FILING DATE: 2001-04-02  
PRIOR APPLICATION NUMBER: US 08/935,377  
PRIOR FILING DATE: 1997-09-22  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 3  
LENGTH: 75  
TYPE: DNA  
ORGANISM: synthetic construct  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (52)..(75)  
US-09-822-250-3

Query Match 100.0%; Score 75; DB 10; Length 75;  
Best Local Similarity 100.0%; Pred. No. 2.3e-12;  
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCCAAAATGAAATTTATTTTGGATATAAAGCGCGCCATGCGCCG 60  
Db 1 GGCCAAAATGAAATTTATTTTGGATATAAAGCGCGCCATGCGCCG 60  
Qy 61 GGCGCAACGCGGA 75  
Db 61 GGCGCAACGCGGA 75  
RESULT 2  
US-09-987-456-142  
Sequence 142, Application US/09987456  
Patent No. US20020123057A1  
GENERAL INFORMATION:  
APPLICANT: University of Rochester

RESULT 4, 5  
US-09-822-250-26/c  
; Sequence 26, Application US/09822250

ORGANISM: synthetic construct

US-09-822-250-33

Query Match  
Best Local Similarity 51.2%; Score 38.4; DB 10; Length 77;  
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 AAAAATGAAATTTATTTTGTGAAATATAAC 44  
DB 77 AAAAATGAAATTTATTTTGTGAAATATAAC 38

RESULT 7

US-09-822-250-1  
; Sequence 1, Application US/09822250  
; Patent No. US20020018785A1  
; GENERAL INFORMATION:  
; APPLICANT: Zauderer, Maurice  
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus  
; FILE REFERENCE: 1821.0010001  
; CURRENT APPLICATION NUMBER: US/09/822,250  
; PRIOR FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: US 08/935,377  
; PRIOR FILING DATE: 1997-09-22  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 69  
; TYPE: DNA  
; ORGANISM: synthetic construct  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (46)..(69)  
US-09-822-250-1

Query Match  
Best Local Similarity 49.3%; Score 37; DB 10; Length 69;  
Matches 59; Conservative 0; Mismatches 10; Indels 6; Gaps 1;

OY 1 GCCCAAAATTTGAAATTTTGTGAAATATAACGCCCGCATGGCCCG 60  
DB 1 GCCCAAAATTTGAAATTTGATCTATTATG-----CACGGCGCGCATGGCCCG 54  
OY 61 GCCGCAACGGCGGA 75  
DB 55 GCCGCAACGGCGGA 69

RESULT 8

US-09-987-456-140  
; Sequence 140, Application US/09987456.  
; Patent No. US20020123057A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Rochester  
; APPLICANT: Zauderer, Maurice  
; APPLICANT: Ernest S. Smith  
; TITLE OF INVENTION: In Vitro Methods of Producing and Selecting  
; FILE REFERENCE: 1821.0070004  
; CURRENT APPLICATION NUMBER: US/09/987,456  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/271,424  
; PRIOR FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: 60/262,067  
; PRIOR FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: 60/298,087  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/249,268  
; PRIOR FILING DATE: 2000-11-17  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 140  
; LENGTH: 69  
; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: p7.5/tk promoter

; NAME/KEY: CDS

; LOCATION: (46)..(69)

; OTHER INFORMATION:

US-09-987-456-140

Query Match  
Best Local Similarity 49.3%; Score 37; DB 10; Length 69;  
Matches 59; Conservative 0; Mismatches 10; Indels 6; Gaps 1;

OY 1 GCCCAAAATTTGAAATTTTGTGAAATATAACGCCCGCATGGCCCG 60  
DB 1 GCCCAAAATTTGAAATTTGATCTATTATG-----CACGGCGCGCATGGCCCG 54  
OY 61 GCCGCAACGGCGGA 75  
DB 55 GCCGCAACGGCGGA 69

RESULT 9

US-09-954-456-2257  
; Sequence 2257, Application US/09954456  
; Patent No. US20020115057A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Paul  
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C  
; FILE REFERENCE: 689290-76  
; CURRENT APPLICATION NUMBER: US/09/954,456  
; PRIOR FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: US/60/233,617  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/60/234,052  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,923  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,134  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,637  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US/60/235,638  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US/60/235,711  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US/60/235,720  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US/60/235,840  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US/60/235,863  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 2276  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2257  
; LENGTH: 62944  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-954-456-2257

Query Match  
Best Local Similarity 39.5%; Score 29.6; DB 10; Length 62944;  
Matches 41; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

OY 3 CCAAAATTTGAAATTTTGTGAAATATAACGCCCGCATGGCCCG 62  
DB 30903 CAAAGATTAATTTCTTTTGTGAAATGAGCTCACTCCATGCGCAGGC 30962

RESULT 10

US-09-764-877-2928  
; Sequence 2928, Application US/09764877  
; Patent No. US20020147140A1

```

US-09-764-864-1695

Query Match          37.1%, Score 27.8; DB 10; Length 21045;
Best Local Similarity 65.1%; Pred. No. 60;
Matches 41; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY      2   GCCAAATTTGAATTATTTTTTTTTTGGAATATAAGCGCGCCGCAATGGGCCGG 61
        ||| ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 18635 GCCTAATTCATAAATTCCTTTTTTTTTTTTGACAGCAGGTTCCTCATTTGCCACAG 18694

QY      62 CCG 64
        || |
DB 18695 CTG 18697


RESULT 13
US-09-764-877-3158
; Sequence 3158, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3158
; LENGTH: 17784
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3158

Query Match          36.3%; Score 27.2; DB 10; Length 17784;
Best Local Similarity 64.1%; Pred. No. 84;
Matches 41; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY      1   GGCAAATAATGAAATTTATTTTTTTTTTGGAAATATAAGCGCGCCGATGGCCCCG 60
        ||| ||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1712  GCGAAATAATGGAATTTTTTTTTTTTTTTTGGAGATATAGATCTCACTCTGTGCCTAG 1771

QY      61 GCCG 64
        || |
DB 1772  GCTG 1775


RESULT 14
US-09-867-701-8272/C
; Sequence 8272, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Hallocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8272
; LENGTH: 338
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-8272

Query Match          35.7%; Score 26.8; DB 10; Length 338;
Best Local Similarity 81.6%; Pred. No. 44;
Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      8   AATTGAAATTTATTTTTTTTTTTTGGAAATATAAGCG 45

```

Db 199 AATTAAATTTTGTGAGACAGCG 162

## RESULT 15

US-09-969-373-257  
; Sequence 257, Application US/09969373  
; Patent No. US20020133852A1  
; GENERAL INFORMATION:  
; APPLICANT: Eifert, Roger J.  
; APPLICANT: Hauge, Brian M.  
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
; FILE REFERENCE: 38-10(52679)A  
; CURRENT APPLICATION NUMBER: US/09/969,373  
; CURRENT FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 09/754,853  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 09/760,427  
; PRIOR FILING DATE: 2001-01-13  
; PRIOR APPLICATION NUMBER: US 09/855,768  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 4593  
; SEQ ID NO 257  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-969-373-257

Query Match 35.7%; Score 26.8; DB 10; Length 468;  
Best Local Similarity 81.6%; Pred. No. 47;  
Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 4 CAAAAATGAAATTTATTTTGGATATTA 41  
DB 246 CAAAAATGAAATTTATTTTATTTATTTATTTA 283

Search completed: November 10, 2002, 11:33:43  
Job time : 43.6657 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:43:30 ; Search time 19.2279 Seconds  
(without alignments)  
1196.219 Million cell updates/sec

Title: US-08-935-377-3

Perfect score: 75  
Sequence: 1 GGGCCAAAATTGAATTTTA.....GCCCGGCCGCCACGGCGGA 75

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2.6/ptodata/1/ina/5A.COMB.seq:\*  
2: /cgn2.6/ptodata/1/ina/5B.COMB.seq:\*  
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5: /cgn2.6/ptodata/1/ina/PCrTus.COMB.seq:\*  
6: /cgn2.6/ptodata/1/ina/Backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39.6	52.8	6474	US-08-651-472-66	Sequence 66, Appl
2	39.6	52.8	6474	US-08-358-928-66	Sequence 66, Appl
3	38.8	51.7	5532	US-08-651-472-72	Sequence 72, Appl
4	38.8	51.7	5532	US-08-358-928-72	Sequence 72, Appl
5	38.4	51.2	49	US-08-651-472-70	Sequence 70, Appl
6	38.4	51.2	49	US-08-358-928-70	Sequence 70, Appl
7	38.4	51.2	6811	US-08-651-472-67	Sequence 67, Appl
8	38.4	51.2	6811	US-08-358-928-67	Sequence 67, Appl
9	38.2	50.9	7252	US-09-238-356-27	Sequence 27, Appl
10	38.2	50.9	7387	US-09-238-356-28	Sequence 28, Appl
11	38	50.7	51	US-08-651-472-56	Sequence 56, Appl
12	38	50.7	51	US-08-358-928-56	Sequence 56, Appl
13	38	50.7	53	US-08-651-472-57	Sequence 57, Appl
14	38	50.7	53	US-08-358-928-57	Sequence 57, Appl
15	38	50.7	3878	US-08-651-472-65	Sequence 65, Appl
16	38	50.7	3878	US-08-358-928-65	Sequence 65, Appl
17	27.2	36.3	12597	US-09-705-289-12	Sequence 12, Appl
18	27	36.0	46	US-08-232-463-40	Sequence 40, Appl
19	27	36.0	63	US-07-750-080A-11	Sequence 11, Appl
20	27	36.0	88	US-07-750-080A-11	Sequence 11, Appl
21	27	36.0	88	US-08-651-472-11	Sequence 11, Appl
22	27	36.0	88	US-08-358-928-11	Sequence 11, Appl
23	27	36.0	92	US-07-750-080A-12	Sequence 12, Appl
24	27	36.0	92	US-08-651-472-12	Sequence 12, Appl
25	27	36.0	92	US-08-358-928-12	Sequence 12, Appl
26	27	36.0	9890	US-08-232-463-18	Sequence 18, Appl
27	26.6	35.5	97	US-07-750-080A-41	Sequence 41, Appl

C 28	26.6	35.5	97	3	US-08-651-472-41	Sequence 41, Appl
C 29	26.6	35.5	97	4	US-08-358-928-41	Sequence 41, Appl
C 30	26.6	35.5	134	1	US-07-750-080A-14	Sequence 14, Appl
C 31	26.6	35.5	134	3	US-08-651-472-14	Sequence 14, Appl
C 32	26.6	35.5	134	4	US-08-358-928-14	Sequence 14, Appl
C 33	26.6	35.5	4145	3	US-08-651-472-62	Sequence 62, Appl
C 34	26.6	35.5	4145	4	US-08-358-928-62	Sequence 62, Appl
C 35	26	34.7	1000	2	US-08-747-121-20	Sequence 20, Appl
C 36	26	34.7	2002	2	US-08-747-121-1	Sequence 1, Appl
C 37	25.8	34.4	90	4	US-09-065-058-16	Sequence 16, Appl
C 38	25.6	34.1	785	4	US-09-185-244-9	Sequence 9, Appl
C 39	25.6	34.1	785	4	US-09-471-913-4	Sequence 4, Appl
C 40	25.6	34.1	1279	4	US-09-185-244-2	Sequence 2, Appl
C 41	25.6	34.1	1279	4	US-09-471-913-6	Sequence 6, Appl
C 42	25.4	33.9	3471	2	US-08-715-568A-2	Sequence 2, Appl
C 43	25.2	33.6	55	1	US-07-750-080A-38	Sequence 38, Appl
C 44	25.2	33.6	55	1	US-07-750-080A-39	Sequence 39, Appl
C 45	25.2	33.6	55	3	US-08-651-472-38	Sequence 38, Appl

## ALIGNMENTS

RESULT 1  
US-08-651-472-66/c  
Sequence 66, Application US/08651472

Patent No. 6103244  
GENERAL INFORMATION:

APPLICANT: DORNER, Friedrich

APPLICANT: SCHREIFLINGER, Friedrich

APPLICANT: FALKNER, Falko Gunter

APPLICANT: FLEIDERER, Michael

TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC

TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1

NUMBER OF INVENTION: (HIV-1) ANTIGENS

NUMBER OF SEQUENCES: 95

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM: disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/651,472

FILING DATE: 435

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/914,738

FILING DATE: 20-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/750,080

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 30472/166/IMMU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 66:

SEQUENCE CHARACTERISTICS:

LENGTH: 6474 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid:

DESCRIPTION: Synthetic DNA oligonucleotide  
IMMEDIATE SOURCE:  
CLONE: pselp-9p160M  
US-08-651-472-66

Query Match 52.8%; Score 39.6; DB 3; Length 6474;  
Best Local Similarity 83.3%; Pred. No. 0.0032;  
Matches 45; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 5 AAAAATGAAATTTATTTTGTGCAATATAAGCGCCGCGCATGGGCC 58  
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Db 3964 AAAAATGAAATTTATTTTGTGCAATATAAGCGCCGCGCATGGGCC 3911

## RESULT 2

US-08-358-928-66/c  
Sequence 66, Application US/08358928  
Patent No. 6265183  
GENERAL INFORMATION:  
APPLICANT: DORNER, Friedrich  
APPLICANT: SCHEFLINGER, Friedrich  
APPLICANT: FALKNER, Falko Gunter  
APPLICANT: FLEIDERER, Michael  
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC  
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/358, 928  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/914, 738  
FILING DATE: 20-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/750, 080  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/166/IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6474 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid;  
DESCRIPTION: Synthetic DNA oligonucleotide  
IMMEDIATE SOURCE:  
CLONE: pselp-9p160M  
US-08-358-928-66

Query Match 52.8%; Score 39.6; DB 4; Length 6474;  
Best Local Similarity 83.3%; Pred. No. 0.0032;  
Matches 45; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 5 AAAAATGAAATTTATTTTGTGCAATATAAGCGCCGCGCATGGGCC 58  
|||||  
Db 3964 AAAAATGAAATTTATTTTGTGCAATATAAGCGCCGCGCATGGGCC 3911

RESULT 3  
US-08-651-472-72/c  
Sequence 72, Application US/08651472  
Patent No. 6103244

GENERAL INFORMATION:  
APPLICANT: DORNER, Friedrich  
APPLICANT: SCHEFLINGER, Friedrich  
APPLICANT: FALKNER, Falko Gunter  
APPLICANT: FLEIDERER, Michael  
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC  
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/651,472  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/914,738  
FILING DATE: 20-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/750,080  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/166/IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 72:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5532 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid;  
DESCRIPTION: Synthetic DNA oligonucleotide  
IMMEDIATE SOURCE:  
CLONE: DN29p1a-FIX  
US-08-651-472-72

Query Match 51.7%; Score 38.8; DB 3; Length 5532;  
Best Local Similarity 79.3%; Pred. No. 0.0053;  
Matches 46; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 3 CCAAATGAAATTTATTTTGTGCAATATAAGCGCCGCGCATGGGCCG 60  
|||||  
Db 3709 CTAATAATGAAATTTATTTTGTGCAATATAAGCGCCGCGCATGGACG 3652

RESULT 4  
US-08-358-928-72/c  
Sequence 72, Application US/08358928  
Patent No. 6265183

```
GENERAL INFORMATION:
APPLICANT: DORNER, Friedrich
APPLICANT: SCHEIFLINGER, Friedrich
APPLICANT: FALKNER, Falko Gunter
APPLICANT: PELEIDERER, Michael
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
TITLE OF INVENTION: (HIV-1) ANTIGENS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,928
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,738
FILING DATE: 20-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/166/IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 5532 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
CLONE: PN29pta-FIX
US-08-358-928-72

Query Match          51.7%; Score 38.8; DB 4; Length 5532;
Best Local Similarity 79.3%; Pred. No. 0.0053;
Matches 46; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 3 CCAAAATGGAATTTTATTTTGGATATTAAGCGCGCCATGGCGCCG 60
DB 3709 CTAATAATGGAATTTTATTTTGGATATTAAGCGCTCCATGGAGCG 3652

RESULT 5
US-08-651-472-70
Sequence 70, Application US/08651472
Patent No. 6103244
GENERAL INFORMATION:
APPLICANT: DORNER, Friedrich
APPLICANT: SCHEIFLINGER, Friedrich
APPLICANT: FALKNER, Falko Gunter
APPLICANT: PELEIDERER, Michael
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
TITLE OF INVENTION: (HIV-1) ANTIGENS
NUMBER OF SEQUENCES: 95
```

```
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,472
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,738
FILING DATE: 20-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/166/IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
CLONE: self promoter
US-08-651-472-70

Query Match          51.2%; Score 38.4; DB 3; Length 49;
Best Local Similarity 97.5%; Pred. No. 0.0022;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCAAAATGGAATTTTATTTTGGATATTAAGCGCGCCATGGCGCCG 42
DB 9 CTAATAATGGAATTTTATTTTGGATATTAAGCGCTCCATGGAGCG 48

RESULT 6
US-08-358-928-70
Sequence 70, Application US/08358928
Patent No. 6265183
GENERAL INFORMATION:
APPLICANT: DORNER, Friedrich
APPLICANT: SCHEIFLINGER, Friedrich
APPLICANT: FALKNER, Falko Gunter
APPLICANT: PELEIDERER, Michael
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
TITLE OF INVENTION: (HIV-1) ANTIGENS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
```

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,928
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,738
FILING DATE: 20-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/166/1MMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTOR: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
CLONE: self promoter

```

```

:
: TELEPHONE: (202)672-5300
:
: TELEFAX: (202)672-5399
:
: TELEX: 904136
:
: INFORMATION FOR SEQ ID NO: 67:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 6811 base pairs
:
: TYPE: nucleic acid
:
: STRANDEDNESS: single
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: Other nucleic acid;
:
: DESCRIPTION: Synthetic DNA oligonucleotide
:
: IMMEDIATE SOURCE:
:
: CLONE: pN2-9p1a Prots
:
US-08-358-928-67

Query Match
Best Local Similarity 97.5%; Score 38.4; DB 4; Length 6811;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCAAAATGAAATTTATTTTGTGGAATATAA 42
Db 4988 CTAATAATGAAATTTATTTTGTGGAATATAA 4949

RESULT 9
US-09-238-356-27/c
: Sequence 27, Application US/09238356
: Patent No. 6312683
:
: GENERAL INFORMATION:
:
: APPLICANT: Kingsman, et al
:
: TITLE OF INVENTION: Retroviral Vectors
:
: FILE REFERENCE: 674523-2006
:
: CURRENT APPLICATION NUMBER: US/09/238,356
:
: PRIOR FILING DATE: 1999-01-27
:
: PRIOR APPLICATION NUMBER: PCT/GB/03876
:
: NUMBER OF SEQ ID NOS: 64
:
: SOFTWARE: PatentIn version 3.0
:
: SEQ ID NO 27
:
: LENGTH: 7252
:
: TYPE: DNA
:
: ORGANISM: Artificial Sequence, plasmid
:
: FEATURE:
:
: NAME/KEY: misc_feature
:
: LOCATION: (1)..(7252)
:
: OTHER INFORMATION: plasmid vector
:
: PUBLICATION INFORMATION:
:
: DATABASE ACCESSION NUMBER: AX003206
:
: DATABASE ENTRY DATE: 2000-08-24
:
: RELEVANT RESIDUES: (1)..(7252)
:
US-09-238-356-27

Query Match
Best Local Similarity 93.0%; Score 38.2; DB 4; Length 7252;
Matches 40; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 AAAAATGAAATTTATTTTGTGGAATATAAGCGC 47
Db 874 AAAAATGAAATTTATTTTGTGGAATATAAATAGC 832

RESULT 10
US-09-238-356-28/c
: Sequence 28, Application US/09238356
: Patent No. 6312683
:
: GENERAL INFORMATION:
:
: APPLICANT: Kingsman, et al
:
: TITLE OF INVENTION: Retroviral Vectors
:
: FILE REFERENCE: 674523-2006
:
: CURRENT APPLICATION NUMBER: US/09/238,356
:
: CURRENT FILING DATE: 1999-01-27
:
: PRIOR APPLICATION NUMBER: PCT/GB/03876
:
: PRIOR FILING DATE: 1998-12-22
```

```

:
: NUMBER OF SEQ ID NOS: 64
:
: SOFTWARE: PatentIn version 3.0
:
: SEQ ID NO 28
:
: LENGTH: 7387
:
: TYPE: DNA
:
: ORGANISM: Artificial Sequence, primer
:
: FEATURE:
:
: NAME/KEY: misc_feature
:
: LOCATION: (1)..(7387)
:
: OTHER INFORMATION: plasmid vector
:
: PUBLICATION INFORMATION:
:
: DATABASE ACCESSION NUMBER: AX003207
:
: DATABASE ENTRY DATE: 2000-08-24
:
: RELEVANT RESIDUES: (1)..(7387)
:
US-09-238-356-28

Query Match
Best Local Similarity 93.0%; Score 38.2; DB 4; Length 7387;
Matches 40; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 AAAAATGAAATTTATTTTGTGGAATATAAGCGC 47
Db 3889 AAAAATGAAATTTATTTTGTGGAATATAAATAGC 3847

RESULT 11
US-08-651-472-56
: Sequence 56, Application US/08651472
: Patent No. 6103244
:
: GENERAL INFORMATION:
:
: APPLICANT: DORNER, Friedrich
:
: APPLICANT: SCHEIFLINGER, Friedrich
:
: APPLICANT: FALKNER, Falko Gunter
:
: APPLICANT: PELEIDERER, Michael
:
: TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
:
: TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
:
: TITLE OF INVENTION: (HIV-1) ANTIGENS
:
: NUMBER OF SEQUENCES: 95
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: Foley & Lardner
:
: STREET: 3000 K Street, N.W., Suite 500
:
: City: Washington
:
: STATE: D.C.
:
: COUNTRY: USA
:
: ZIP: 20007-5109
:
: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: Floppy disk
:
: COMPUTER: IBM PC compatible
:
: OPERATING SYSTEM: PC-DOS/MS-DOS
:
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: US/08/651,472
:
: FILING DATE:
:
: CLASSIFICATION: 435
:
: PRIOR APPLICATION DATA:
:
: APPLICATION NUMBER: US 07/914,738
:
: FILING DATE: 20-JUL-1992
:
: PRIOR APPLICATION DATA:
:
: APPLICATION NUMBER: US 07/750,080
:
: FILING DATE: 26-AUG-1991
:
: ATTORNEY/AGENT INFORMATION:
:
: NAME: BENT, Stephen A.
:
: REGISTRATION NUMBER: 29,768
:
: REFERENCE/DOCKET NUMBER: 30472/166/JMMU
:
: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: (202)672-5300
:
: TELEFAX: (202)672-5399
:
: TELEX: 904136
:
: INFORMATION FOR SEQ ID NO: 56:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 51 base pairs
:
: TYPE: nucleic acid
:
: STRANDEDNESS: single
```

TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid;  
DESCRIPTION: Synthetic DNA oligonucleotide  
IMMEDIATE SOURCE:  
CLONE: o-selp1  
US-08-651-472-56

Query Match 50.7%; Score 38; DB 3; Length 51;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 AAAAATGAAATTTATTTTGGAAATATAA 42  
DB 5 AAAAATGAAATTTATTTTGGAAATATAA 42

## RESULT 12

US-08-358-928-56  
Sequence 56, Application US/08358928  
Patent No. 6265183

GENERAL INFORMATION:  
APPLICANT: DORNER, Friedrich  
APPLICANT: SCHEFFLINGER, Friedrich  
APPLICANT: FALKNER, Falko Gunter  
APPLICANT: PLEIDERER, Michael  
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC  
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/358,928  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/914,738  
FILING DATE: 20-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/750,080  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/166/IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5399  
TELEFAX: 904136  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 51 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid;  
DESCRIPTION: Synthetic DNA oligonucleotide  
IMMEDIATE SOURCE:  
CLONE: o-selp1  
US-08-358-928-56

Query Match 50.7%; Score 38; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 0.003;

Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 5 AAAAATGAAATTTATTTTGGAAATATAA 42  
DB 5 AAAAATGAAATTTATTTTGGAAATATAA 42

## RESULT 13

US-08-651-472-57/c  
Sequence 57, Application US/08651472  
Patent No. 6103244

GENERAL INFORMATION:  
APPLICANT: DORNER, Friedrich  
APPLICANT: SCHEFFLINGER, Friedrich  
APPLICANT: FALKNER, Falko Gunter  
APPLICANT: PLEIDERER, Michael  
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC  
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/651,472  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/914,738  
FILING DATE: 20-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/750,080  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/166/IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 53 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid;  
DESCRIPTION: Synthetic DNA oligonucleotide  
IMMEDIATE SOURCE:  
CLONE: o-selp1  
US-08-651-472-57

Query Match 50.7%; Score 38; DB 3; Length 53;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 AAAAATGAAATTTATTTTGGAAATATAA 42  
DB 51 AAAAATGAAATTTATTTTGGAAATATAA 14

RESULT 14  
US-08-358-928-57/c

```
; Sequence 57, Application US/08358928
; Patent No. 6265183
; GENERAL INFORMATION:
; APPLICANT: DORNER, Friedrich
; APPLICANT: SCHEIFLINGER, Friedrich
; APPLICANT: FALKNER, Falko Gunter
; APPLICANT: FLEIDERER, Michael
; TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
; TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,928
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/914,738
; FILING DATE: 20-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/750,080
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/166/IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: Synthetic DNA oligonucleotide
; IMMEDIATE SOURCE:
; CLONE: o-selpil
US-08-358-928-57

Query Match 50.7%; Score 38; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AAAAATGAAATTTATTTTTCGAATATATA 42
Db 51 AAAAATGAAATTTATTTTTCGAATATATA 14

RESULT 15
US-08-651-472-65/C
; Sequence 65, Application US/08651472
; Patent No. 6103244
; GENERAL INFORMATION:
; APPLICANT: DORNER, Friedrich
; APPLICANT: SCHEIFLINGER, Friedrich
; APPLICANT: FALKNER, Falko Gunter
; APPLICANT: FLEIDERER, Michael
; TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
; TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/651,472
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/914,738
; FILING DATE: 20-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/750,080
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/166/IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3878 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: Synthetic DNA oligonucleotide
; IMMEDIATE SOURCE:
; CLONE: pselp-gpt-L2
US-08-651-472-65

Query Match 50.7%; Score 38; DB 3; Length 3878;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AAAAATGAAATTTATTTTTCGAATATATA 42
Db 1368 AAAAATGAAATTTATTTTTCGAATATATA 1331
```

```
; TITLE OF INVENTION: (HIV-1) ANTIGENS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/651,472
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/914,738
; FILING DATE: 20-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/750,080
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/166/IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3878 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid;
; DESCRIPTION: Synthetic DNA oligonucleotide
; IMMEDIATE SOURCE:
; CLONE: pselp-gpt-L2
US-08-651-472-65

Query Match 50.7%; Score 38; DB 3; Length 3878;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AAAAATGAAATTTATTTTTCGAATATATA 42
Db 1368 AAAAATGAAATTTATTTTTCGAATATATA 1331
```

Search completed: November 10, 2002, 08:36:09  
Job time : 26.2279 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run On: November 10, 2002, 05:05:45 ; Search time 705 Seconds

(Without alignments)  
5985.683 Million cell updates/sec

Title: US-08-935-377-6

Perfect score: 145

Sequence: 1 GCCCAAAATGAAAACTA.....TTGTTTTTGCGCCGCCGCC 145

Scoring table:

IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sls:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_scs:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145	100.0	145	6 AX326743	AX326743 Sequence
2	132	91.0	148	6 AX326744	AX326744 Sequence
3	131	90.3	149	6 AX326745	AX326745 Sequence
4	130	89.7	150	6 AX326746	AX326746 Sequence
5	70.8	48.8	4326	5 AF072997	AF072997 Cloning v
6	70.4	48.6	5255	2 AF309793	AF309793 Clupea pa
7	70.4	48.6	5592	6 AR205969	AR205969 Sequence
8	70.2	48.4	656	5 AF309795	AF309795 Clupea pa
9	69.4	47.9	13558	6 AX287041	AX287041 Sequence
10	69	47.6	424	6 A44281	A44281 Sequence 9
11	69	47.6	259	6 AX284796	AX284796 Sequence
12	69	47.6	2059	12 AY034154	AY034154 Cloning v
13	69	47.6	2850	9 AB035274	AB035274 Homo sapi
14	69	47.6	2958	6 AX247548	AX247548 Sequence
15	69	47.6	2958	12 ARBLKSM	X52326 pbuescript
16	69	47.6	2958	12 ARBLKSP	X52329 pbuescript
17	69	47.6	2961	12 ARBL2KSM	X53327 pbuescript
18	69	47.6	2961	12 ARBL2KSP	X53329 pbuescript
19	69	47.6	2964	12 SYNBLKSMV	L08784 Bluescribe
20	69	47.6	2964	12 SYNBLKSPV	L08785 Bluescribe
21	69	47.6	3306	12 SYNBLKSPV	D85525 Cloning vec
22	69	47.6	3417	12 AF153422	AF153422 Cloning v
23	69	47.6	3485	12 AF178449	AF178449 Integrati
24	69	47.6	4144	12 XX035131	U35131 Plasmid pBS
25	69	47.6	4267	12 PRS304	U03436 Yeast integ
26	69	47.6	4289	12 XX035136	U35136 Plasmid pBS
27	69	47.6	4373	12 PRS306	U03438 Yeast integ
28	69	47.6	4443	12 PRS303	U03435 Yeast integ
29	69	47.6	4549	12 AF178452	AF178452 Integrati
30	69	47.6	4670	12 ASAJ5326	AJ005326 pGAL1(+)
31	69	47.6	4670	12 ASAJ5329	AJ005329 pGAL1(-)
32	69	47.6	4707	12 XX002374	U02374 Cloning vec
33	69	47.6	4768	12 XX025061	U25061 Cloning vec
34	69	47.6	4783	12 PRS314	U03440 Yeast centr
35	69	47.6	4887	12 PRS316	U03442 Yeast centr
36	69	47.6	4950	12 XX025060	U25060 Cloning vec
37	69	47.6	4967	12 PRS313	U03439 Yeast centr
38	69	47.6	5144	12 CV023751	U23751 Cloning vec
39	69	47.6	5187	12 U34887	U34887 Yeast integ
40	69	47.6	5228	12 XX025059	U25059 Cloning vec
41	69	47.6	5504	12 PRS305	U03437 Yeast integ
42	69	47.6	5634	12 CV014125	U14125 Cloning vec
43	69	47.6	5973	12 AF504908	AF504908 Cloning v
44	69	47.6	6018	12 PRS315	U03441 Yeast centr
45	69	47.6	6340	12 ASAJ5323	AJ005323 pCP1(-) K

## ALIGNMENTS

RESULT 1  
AX326743  
LOCUS AX326743 145 bp DNA PAT 07-JAN-2002  
DEFINITION Sequence 4 from Patent WO01/2995.  
ACCESSION AX326743  
VERSION AX326743.1 GI.18097469  
KEYWORDS  
SOURCE Synthetic construct.  
ORGANISM Synthetic construct.  
REFERENCE 1  
Zaenderer, M. and Smith, E. S.  
AUTHORS Methods of producing a library and methods of selecting  
TITLE polynucleotides of interest  
JOURNAL Patent: WO 01/2995-A 4 04-OCT-2001.

UNIVERSITY OF ROCHESTER (US)  
FEATURES  
source  
1. 145  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Nucleotide Sequence of p7.5/ATG0/Lk"  
BASE COUNT 34 a 37 c 38 g 36 t  
ORIGIN

Query Match  
Best Local Similarity 100.0%; Score 145; DB 6; Length 145;  
Pred. No. 8e-36;  
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGCCAAAATTGAAAACCTAGATCTATTATTCACGCGCGCCCGGATCCCCCGGCG 60  
|||||  
DB 1 GGCCAAAATTGAAAACCTAGATCTATTATTCACGCGCGCCCGGATCCCCCGGCG 60  
|||||

OY 61 TGCAGGAATTCGATATCAAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAATCAAC 120  
|||||  
DB 61 TGCAGGAATTCGATATCAAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAATCAAC 120  
|||||

OY 121 TAATTTTGTGTTTGTGGCGCGCC 145  
|||||  
DB 121 TAATTTTGTGTTTGTGGCGCGCC 145  
|||||

RESULT 2  
AX326744 148 bp DNA linear PAT 07-JAN-2002  
LOCUS  
DEFINITION Sequence 5 from Patent W00172995.  
ACCESSION AX326744  
VERSION AX326744.1 GI:18097470  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct.  
synthetic construct.  
artificial sequences.  
REFERENCE  
1  
AUTHORS Zauderer, M. and Smith, E.S.  
TITLE Methods of producing a library and methods of selecting polynucleotides of interest  
JOURNAL Patent: WO 0172995-A 5 04-OCT-2001;  
UNIVERSITY OF ROCHESTER (US)  
FEATURES  
source  
1. 148  
Location/Qualifiers  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Nucleotide Sequence of p7.5/ATG1/Lk"  
BASE COUNT 35 a 37 c 39 g 37 t  
ORIGIN

Query Match  
Best Local Similarity 98.0%; Score 132; DB 6; Length 148;  
Pred. No. 1.2e-31;  
Matches 145; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

OY 1 GGCCAAAATTGAAAACCTAGATCTATTATTCACGCGCGCCCGGATCCCCCGG 57  
|||||  
DB 1 GGCCAAAATTGAAAACCTAGATCTATTATTCACGCGCGCCCGGATCCCCCGG 60  
|||||

OY 58 GGCTCGAGGAATTCGATATCAAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAAT 117  
|||||  
DB 61 GGCTCGAGGAATTCGATATCAAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAAT 120  
|||||

OY 118 AACTAATTTGTTTGTGGCGCGCC 145  
|||||  
DB 121 AACTAATTTGTTTGTGGCGCGCC 148  
|||||

RESULT 3  
AX326745 149 bp DNA linear PAT 07-JAN-2002  
LOCUS  
DEFINITION Sequence 6 from Patent W00172995.  
ACCESSION AX326745  
VERSION AX326745.1 GI:18097471

KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct.  
synthetic construct.  
artificial sequences.  
REFERENCE  
1  
AUTHORS Zauderer, M. and Smith, E.S.  
TITLE Methods of producing a library and methods of selecting polynucleotides of interest  
JOURNAL Patent: WO 0172995-A 6 04-OCT-2001;  
UNIVERSITY OF ROCHESTER (US)  
FEATURES  
source  
1. 149  
Location/Qualifiers  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Nucleotide Sequence of p7.5/ATG2/Lk"  
BASE COUNT 36 a 37 c 39 g 37 t  
ORIGIN

Query Match  
Best Local Similarity 90.3%; Score 131; DB 6; Length 149;  
Pred. No. 2.5e-31;  
Matches 145; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

OY 1 GGCCAAAATTGAAAACCTAGATCTATTATTCACGCGCGCCCGGATCCCCCG 56  
|||||  
DB 1 GGCCAAAATTGAAAACCTAGATCTATTATTCACGCGCGCCCGGATCCCCCG 60  
|||||

OY 57 GGCTCGAGGAATTCGATATCAAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAAT 116  
|||||  
DB 61 GGCTCGAGGAATTCGATATCAAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAAT 120  
|||||

OY 117 TAATTAATTTGTTTGTGGCGCGCC 145  
|||||  
DB 121 TAATTAATTTGTTTGTGGCGCGCC 149  
|||||

RESULT 4  
AX326746 150 bp DNA linear PAT 07-JAN-2002  
LOCUS  
DEFINITION Sequence 7 from Patent W00172995.  
ACCESSION AX326746  
VERSION AX326746.1 GI:18097472  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct.  
synthetic construct.  
artificial sequences.  
REFERENCE  
1  
AUTHORS Zauderer, M. and Smith, E.S.  
TITLE Methods of producing a library and methods of selecting polynucleotides of interest  
JOURNAL Patent: WO 0172995-A 7 04-OCT-2001;  
UNIVERSITY OF ROCHESTER (US)  
FEATURES  
source  
1. 150  
Location/Qualifiers  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Nucleotide Sequence of p7.5/ATG3/Lk"  
BASE COUNT 36 a 38 c 39 g 37 t  
ORIGIN

Query Match  
Best Local Similarity 89.7%; Score 130; DB 6; Length 150;  
Pred. No. 5.3e-31;  
Matches 145; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

OY 1 GGCCAAAATTGAAAACCTAGATCTATTATTCACGCGCGCCCGGATCCCCCG 55  
|||||  
DB 1 GGCCAAAATTGAAAACCTAGATCTATTATTCACGCGCGCCCGGATCCCCCG 60  
|||||

OY 56 CGGCTCGAGGAATTCGATATCAAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAA 115  
|||||  
DB 61 CGGCTCGAGGAATTCGATATCAAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAA 120  
|||||

OY 116 CTAATTAATTTGTTTGTGGCGCGCC 145  
|||||

Db 121 CTAACATAATTTGTTTGTGGGCCGCCGCC 150

RESULT 5  
LOCUS AF072997 4326 bp DNA circular SYN 02-JUL-1998  
DEFINITION Cloning vector pCMWTA3a, complete sequence.  
ACCESSION AF072997  
VERSION AF072997.1 GI:3284001  
KEYWORDS  
ORGANISM Cloning vector pCMWTA3a.  
SOURCE Cloning vector pCMWTA3a.  
REFERENCE 1 (bases 1 to 4326)  
AUTHORS Lu, Q.  
TITLE pCMWTA3a  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 4326)  
AUTHORS Lu, Q.  
TITLE Direct Submission  
JOURNAL Submitted (22-JUN-1998) Technical Services, Stratagene, 11011 N.  
Torrey Pines Rd., San Diego, CA 92037, USA  
FEATURES  
source 1..4326  
/organism="Cloning vector pCMWTA3a"  
/db\_xref="taxon:78249"  
/lab\_host="Escherichia coli K12"  
1..602  
/note="CMV promoter"  
713..799  
/note="multiple cloning site"  
859..1242  
/note="SV40 poly a signal region"  
1242..1703  
/note="f1 origin of replication"  
1704..1835  
/note="Pbla promoter"  
1836..2227  
/note="SV40 origin of replication"  
2228..3022  
/function="kanamycin resistance"  
/codon\_start=1  
/transl\_table=1  
/product="aminoglycoside phosphotransferase"  
/protein\_id="AAC25426.1"  
/db\_xref="GI:3284002"  
/translation="MIEDDGLHAGSPAWEKFLGYDMAOQTIGCDAAVFRISAQR  
PVLFEKTDLSGALNLEDEARLSMLATGVPCAIVDVTEAGRDMLLGEVGGDL  
LSHLAPAEKYSIMADAMRRLHTLDPATCEPDHAKHRIERARPMRAGVDDDDLE  
EHGCLAPAELEFARLAKASMPGCEDEVTHGACLPINIVENGSRSGFTDCGRIGVADRY  
ODIALATRDIAEELGEMADRFVLVYGIAPDSORIAFYRLDDEF"  
3469..4316  
/note="ColE1 origin of replication"  
BASE COUNT 1056 a 1116 c 1107 g 1047 t  
ORIGIN

Query Match 48.8%; Score 70.8; DB 12; Length 4326;  
Best Local Similarity 76.3%; Pred. No. 8.9e-12;  
Matches 87; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Db 681 GCAGAACTCACTCTGAGAGAGATCTGGCCCGGCGGATCCCGGCTCGAGGAATTC 740

Db 72 GATATCAAGCTTATGATACCGCTGACCTCGAGGGGGGGCTTAACCTAATT 125  
|||||  
741 GATATCAAGCTTATGATACCGCTGACCTCGAGGGGGGGCGGACTTAATT 794  
|||||

RESULT 6  
LOCUS AF309793 525 bp DNA linear VRT 23-JAN-2002  
DEFINITION Clupea pallasi microsatellite Chai13 sequence.

ACCESSION AF309793  
VERSION AF309793.1 GI:12060921  
KEYWORDS  
SOURCE Clupea pallasi.  
ORGANISM Clupea pallasi.  
REFERENCE 1 (bases 1 to 525)  
AUTHORS Miller, K.M., Laboree, K., Schulze, A.D. and Kaukinen, K.H.  
TITLE Development of microsatellite loci in Pacific herring (Clupea pallasi)  
JOURNAL Mol. Ecol. Notes 1 (3), 131-132 (2001)  
REFERENCE 2 (bases 1 to 525)  
AUTHORS Miller, K.M., Laboree, K. and Kaukinen, K.  
TITLE Direct Submission  
JOURNAL Submitted (02-OCT-2000) Aquaculture/Genetics, Pacific Biological Station, Hammond Bay Rd., Nanaimo, B.C. V9R 5K6, Canada  
FEATURES  
source 1..525  
/organism="Clupea pallasi"  
/db\_xref="taxon:30724"  
/clone="Chai13"  
repeat\_region 1..525  
/note="microsatellite Chai13"  
/rpt\_type=tandem  
BASE COUNT 130 a 136 c 166 g 93 t  
ORIGIN

Query Match 48.6%; Score 70.4; DB 5; Length 525;  
Best Local Similarity 79.8%; Pred. No. 8.7e-12;  
Matches 83; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Db 126 TTGATCGAGACACCCGACACAGATCCCGGCGTGCAGGAATTCGATACAGCTTATC 67  
|||||

Db 87 GATACCGTGCACCTCGAGGGGGCCCTAATACTAATTTTGT 130  
|||||

Db 66 GATACCGTGCACCTCGAGGGGGCCCGACGATCCAGCTTTTGT 23  
|||||

RESULT 7  
LOCUS AR205969 5592 bp DNA linear PAT 20-JUN-2002  
DEFINITION Sequence 37 from patent US 6369296.  
ACCESSION AR205969  
VERSION AR205969.1 GI:21503686  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 5592)  
AUTHORS Ratcliff, F. Giles., Martin-Hernandez, A. Montserrat. and Baulcombe, D. Charles.  
TITLE Recombinant plant viral vectors  
JOURNAL Patent: US 6369296-A 37 09-APR-2002;  
FEATURES Location/Qualifiers  
source 1..5592  
/organism="unknown"  
BASE COUNT 1517 a 1318 c 1276 g 1481 t  
ORIGIN

Query Match 48.6%; Score 70.4; DB 6; Length 5592;  
Best Local Similarity 79.8%; Pred. No. 1.2e-11;  
Matches 83; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Db 9 ATGAAAACTAGATCTAATTATTCACAGCGCGCCCGCTGATCCCGGCGCTGCAGGAA 68  
|||||

Db 2514 ATTTAGAGAGCTGAACTCTGATGATCTTAAGATAGTAACTAGTGATCCCGGCTGCAGGAA 2573  
|||||

Db 69 TTGATATCAAGCTTATGATACCGCTGACCTCGAGGGGGGCC 112  
|||||

Db 2574 TTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCC 2617

RESULT 8  
LOCUS AF309795 656 bp DNA linear VRT 23-JAN-2002

DEFINITION Clupea pallasi microsatellite Chai20 sequence.  
ACCESSION AF309795  
VERSION AF309795.1 GI:12060923

KEYWORDS  
SOURCE Clupea pallasi.

ORGANISM

Clupea pallasi  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;  
Clupea.

REFERENCE 1 (bases 1 to 656)

AUTHORS Miller,K.M., Laboree,K., Schulze,A.D. and Kaukinen,K.H.

TITLE Development of microsatellite loci in Pacific herring (Clupea

palasi)

JOURNAL Mol. Ecol. Notes 1 (3), 131-132 (2001)

REFERENCE 2 (bases 1 to 656)

AUTHORS Miller,K.M., Laboree,K. and Kaukinen,K.

TITLE Direct Submission

JOURNAL Submitted (02-OCT-2000) Aquaculture/Genetics, Pacific Biological

Station, Hammond Bay Rd., Nanaimo, B.C. V9R 5K6, Canada

FEATURES  
Location/Qualifiers

1..656

/organism="Clupea pallasi"

/db\_xref="taxon:30724"

/clone="Chai20"

/note="microsatellite Chai20"

repeat\_region

1..656

/rpt\_type=tandem

BASE COUNT 170 a 205 c 142 g 139 t

ORIGIN

Query Match 48.4%; Score 70.2; DB 5; Length 656;

Best Local Similarity 85.7%; Pred. No. 1e-11;

Matches 78; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 40 GCGCGCGTGAATCCCGCGGCGTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACC 99

Db 544 GGAGCCATGATGATCCCGCGGCGTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACC 603

QY 100 TCGAGGGGGGGCGCTTAATTAATTTGTT 130

Db 604 TCGAGGGGGGGCGCGCTTAATTAATTTGTT 634

RESULT 9

AX287041 13558 bp DNA linear PAT 21-NOV-2001

LOCUS AX287041

DEFINITION Sequence 5 from Patent WO0181623.

ACCESSION AX287041

VERSION AX287041.1 GI:17049037

KEYWORDS

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Goetz,B., Kammandel,B., Kuner,R., Scheek,S. and Hiemisch,H.

TITLE Novel neuronally expressed protein and use thereof

JOURNAL Patent: WO 0181623-A 5 01-NOV-2001;

BASEF-LYNX Bioscience AG (DE)

FEATURES

Location/Qualifiers

1..13558

/organism="Mus musculus"

/db\_xref="taxon:10090"

BASE COUNT 2936 a 3419 c 3606 g 3544 t 53 others

ORIGIN

Query Match 47.9%; Score 69.4; DB 6; Length 13558;

Best Local Similarity 92.4%; Pred. No. 3e-11;

Matches 73; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 34 CACGGGCGCCGCTGATGCCCGGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCG 93

Db 13475 CCCACCGCAGGCGCTGATGCCCGGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCG 13534

QY 94 TCGACCTCGAGGGGGGGGCC 112

Db 13535 TCGACCTCGAGGGGGGGGCC 13553

RESULT 10

A44281/c 259 bp DNA linear PAT 07-MAR-1997

LOCUS A44281

DEFINITION Sequence 9 from Patent WO9511300.

ACCESSION A44281

VERSION A44281.1 GI:2299115

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified

REFERENCE 1 (bases 1 to 259)

AUTHORS Chandley,A.C., Kun,M., Sharkey,A.M., Hargreave,T.B. and Cooke,H.J.

TITLE AZOOSPERMIA IDENTIFICATION AND TREATMENT

JOURNAL Patent: WO 9511300-A 9 27-APR-1995;

MEDICAL RES COUNCIL (GB)

COMMENT Other publication AU 7947794 950508.

FEATURES

Location/Qualifiers

1..259

/organism="unidentified"

/db\_xref="taxon:32644"

/clone\_lib="MOUSE GENOMIC LIBRARY"

BASE COUNT 67 a 58 c 63 g 69 t 2 others

ORIGIN

Query Match 47.6%; Score 69; DB 6; Length 259;

Best Local Similarity 88.2%; Pred. No. 2.2e-11;

Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 46 GTGATCCCGCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACG 105

Db 112 GTGATCCCGCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACG 53

QY 106 GGGGGCGCTAATTAATTTGTT 130

Db 52 GGGGGCGCGGTACCCAGCTTTGTT 28

RESULT 11

AX284796/c 424 bp DNA linear PAT 20-NOV-2001

LOCUS AX284796

DEFINITION Sequence 601 from Patent WO0179556.

ACCESSION AX284796

VERSION AX284796.1 GI:17045484

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1

AUTHORS Lillie,J., Brown,J.L., Bolt,A. and van Hufel,C.

TITLE Novel genes, compositions and methods for the identification,

assessment, prevention, and therapy of human cancers

JOURNAL Patent: WO 0179556-A 601 25-OCT-2001;

Millennium Predictive Medicine, Inc. (US)

FEATURES

Location/Qualifiers

1..424

/organism="Homo sapiens"

/db\_xref="taxon:9606"

BASE COUNT 87 a 134 c 118 g 85 t

ORIGIN

Query Match 47.9%; Score 69.4; DB 6; Length 13558;

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Query Match          47.6%; Score 69; DB 6; Length 424;
Best Local Similarity 88.2%; Pred. No. 2,4e-11;
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 46 GTGATCCCCCGGCGTGCAGAAATTCGATATCAGCTTATCGATACCGTCGACCTCGAGG 105
    |||||||
Db 104 GTGATCCCCCGGCGTGCAGAAATTCGATATCAGCTTATCGATACCGTCGACCTCGAGG 45
OY 106 GGGGGCCCTAAGTAATTAATTTGTT 130
    |||||||
Db 44 GGGGGCCCGGTACCCAGCTTTGTT 20

RESULT 12
AY034154/c 2059 bp DNA circular SYN 23-JUL-2001
LOCUS AY034154
DEFINITION Cloning vector pIDN4, complete sequence.
ACCESSION AY034154
VERSION AY034154.1 GI:14324126
KEYWORDS
SOURCE Cloning vector pIDN4.
ORGANISM Cloning vector pIDN4
REFERENCE 1 (bases 1 to 2059)
AUTHORS Hamilton,H.L., Schwartz,K.J. and Dillard,J.P.
TITLE Insertion-duplication mutagenesis of neisseria: use in
characterization of DNA transfer genes in the gonococcal genetic
island
JOURNAL J. Bacteriol. 183 (16), 4718-4726 (2001)
MEDLINE 21359313
PUBMED 11466274
REFERENCE 2 (bases 1 to 2059)
AUTHORS Hamilton,H.L., Schwartz,K.J. and Dillard,J.P.
TITLE Direct Submision
JOURNAL Submitted (11-MAY-2001) Medical Microbiology & Immunology,
University of Wisconsin-Madison, 1300 University Avenue, Madison,
WI 53706, USA

FEATURES
source location/Qualifiers
1..2059
/organism="Cloning vector pIDN4"
/db_xref="taxon:161273"
/note="for insertion-duplication mutagenesis in Neisseria"
40..39
/promoter /note="P73"
complement(187..204)
/note="P7"
277..311
stem_loop complement(310..1113)
gene /gene="ermC"
complement(310..1044)
CDS /gene="ermC"
complement(1051..1054)
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1130..1139
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complement(1276..1976)
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Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 46 GTGATCCCCCGGCGTGCAGAAATTCGATATCAGCTTATCGATACCGTCGACCTCGAGG 105
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Db 143 GTGATCCCCCGGCGTGCAGAAATTCGATATCAGCTTATCGATACCGTCGACCTCGAGG 84
OY 106 GGGGGCCCTAAGTAATTAATTTGTT 130
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Db 83 GGGGGCCCGGTACCCAGCTTTGTT 59

RESULT 13
AB035274 2890 bp mRNA linear PRI 12-JUL-2000
LOCUS AB035274
DEFINITION Homo sapiens mRNA for postreplication repair protein hRAD18,
complete cds.
ACCESSION AB035274
VERSION AB035274.1 GI:9890616
KEYWORDS
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (sites)
Tateishi,S., Sakuraba,Y., Masuyama,S., Inoue,H. and Yamazumi,M.
Dysfunction of human Rad18 results in defective postreplication
repair and hypersensitivity to multiple mutagens
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7927-7932 (2000)
2 (bases 1 to 2890)
Tateishi,S., Yamazumi,M. and Inoue,H.
Direct Submision
Submitted (26-NOV-1999) Satoshi Tateishi, Kumamoto University,
Institute of Molecular Embryology; Kubonji 4-24-1, Kumamoto,
Kumamoto 862-0976, Japan (E-mail:tateegp.kumamoto-u.ac.jp,
Tel:81-096-373-6602, Fax:81-096-373-6604)

FEATURES
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CDS
gene

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Best Local Similarity 88.2%; Pred. No. 3.2e-11;
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 46 GTGGATCCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGCTCGACCTCGAGG 105
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DB 2742 GTGGATCCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGCTCGACCTCGAGG 2801
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QY 106 GGGGGCCTTAACCTAATTTTGT 130
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DB 2802 GGGGGCCTTAACCTAATTTTGT 2826
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RESULT 14
AX247548      2958 bp      DNA      linear      PAT 28-SEP-2001
LOCUS
DEFINITION Sequence 1 from Patent WO0166775.
ACCESSION AX247548
VERSION AX247548.1 GI:15862240
KEYWORDS
SOURCE
ORGANISM synthetic construct.
          artificial sequences.
REFERENCE 1 (bases 1 to 2958)
AUTHORS Evans,D.H., Miller,D.O. and Yao,X.D.
TITLE Dna joining method
JOURNAL Patent: WO 0166775-A 1 13-SEP-2001;
          University of Guelph (CA)
FEATURES
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        /note="pDW101"

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Best Local Similarity 88.2%; Pred. No. 3.2e-11;
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 46 GTGGATCCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGCTCGACCTCGAGG 105
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DB 684 GTGGATCCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGCTCGACCTCGAGG 743
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QY 106 GGGGGCCTTAACCTAATTTTGT 130
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DB 744 GGGGGCCTTAACCTAATTTTGT 768
    |||||||

RESULT 15
ARBLKSM      2958 bp      DNA      circular SYN 29-JAN-2002
LOCUS
DEFINITION pBluescript KS(-) vector DNA, phagemid excised from lambda ZAP.
ACCESSION X52326
VERSION X52326.1 GI:58064
KEYWORDS artificial sequence; cloning vector; expression vector; vector.
SOURCE
ORGANISM synthetic construct.
          synthetic construct.
          artificial sequences.
REFERENCE 1
AUTHORS Short,J.M., Fernandez,J.M., Sorge,J.A. and Huse,W.D.
TITLE Lambda ZAP: a bacteriophage lambda expression vector with in vivo
          excision properties
JOURNAL Nucleic Acids Res. 16 (15), 7583-7600 (1988)
MEDLINE 90067967
PUBMED 2555794
REFERENCE 3 (bases 1 to 2958)
AUTHORS Thomas,E.A.
TITLE Direct Submission
JOURNAL Submitted (20-FEB-1990) Thomas E.A., Stratagene Clonin Systems,
          11099 North Torrey Pines Rd., La Jolla, CA 92037, USA
FEATURES
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        /db_xref="taxon:32630"
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Query Match      47.6%; Score 69; DB 12; Length 2958;
Best Local Similarity 88.2%; Pred. No. 3.2e-11;
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 46 GTGGATCCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGCTCGACCTCGAGG 105
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DB 687 GTGGATCCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGCTCGACCTCGAGG 746
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QY 106 GGGGGCCTTAACCTAATTTTGT 130
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DB 747 GGGGGCCTTAACCTAATTTTGT 771
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Search completed: November 10, 2002, 06:52:54
Job time : 713 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:42:15 ; Search time 1305 Seconds

(without alignments)  
1799,499 Million cell updates/sec

Title: US-08-935-377-6

Sequence: 1 GGCCAAAATGAAAACTA.....TTGTTTGTGGCCGCCGCC 145

Scoring table: IDENTITY-NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_man:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rnd:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75.4	52.0	891	14	BQ140386
2	72	49.7	182	13	B1306115
3	72	49.7	793	14	BQ143916
4	70.4	48.6	841	17	CNS06W11
5	70	48.3	536	17	CNS06VAH
6	70	48.3	682	17	AQ074693

7	69.8	48.1	804	14	BQ158468
8	69.6	48.0	355	17	CNS06XBT
9	69.4	47.9	182	13	B1305962
10	69.4	47.9	186	13	B1305695
11	69.2	47.7	574	17	BH001110
12	69.2	47.7	912	17	CNS06UFS
13	69	47.6	162	10	BE428068
14	69	47.6	390	9	AU234451
15	69	47.6	400	9	AU278852
16	69	47.6	864	17	AQ937400
17	68.8	47.4	175	13	B1306167
18	68.8	47.4	182	13	B1306149
19	68.8	47.4	182	13	B1306159
20	68.8	47.4	182	13	B1306178
21	68.8	47.4	182	13	B1306180
22	68.8	47.4	757	14	BQ155148
23	68	46.9	295	10	BE428455
24	68	46.9	608	17	AQ009167
25	67.8	46.8	728	10	AM682547
26	67.6	46.6	216	17	CNS06E50
27	67.6	46.6	829	17	AQ937397
28	67.4	46.5	128	17	CNS07GJ4
29	67.4	46.5	528	17	B69688
30	67.4	46.5	721	17	CNS06DOU
31	67.4	46.5	902	17	CNS06WUM
32	67.2	46.3	198	17	CNS06XOI
33	67.2	46.3	968	17	CNS06V41
34	67	46.2	107	13	BM398556
35	67	46.2	108	10	BE492551
36	67	46.2	108	17	B54292
37	67	46.2	124	10	AW914179
38	67	46.2	141	9	AU037147
39	67	46.2	141	17	B95279
40	67	46.2	144	17	B80294
41	67	46.2	157	12	BF281431
42	67	46.2	159	13	B1306719
43	67	46.2	169	17	AQ013255
44	67	46.2	175	17	AQ041198
45	67	46.2	180	13	B1306345

#### ALIGNMENTS

RESULT 1  
BQ140386  
LOCUS  
DEFINITION  
BQ140386 891 bp mRNA linear EST 26-APR-2002  
NF035A10PH1081 Phoma-infected Medicago truncatula cDNA clone  
NF035A10PH 5', mRNA sequence.

ACCESSION  
BQ140386  
VERSION  
BQ140386.1 GI:20276512  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS

TITLE  
JOURNAL  
COMMENT  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
Medicago truncatula Phoma-infected library  
Unpublished (2002)  
Contact: Paiva NL  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7317  
Fax: 580 221 7380  
Email: nlpaiva@noble.org  
Insert Length: 891 Std Error: 0.00

Plate: 035 row: A column: 10  
Seq primer: TCACACAGGAACAGCTATGAC.  
Location/Qualifiers

FEATURES  
source

1. 891  
/organism="Medicago truncatula"  
/db\_xref="taxon:3880"  
/clone="NF035A10PH"  
/clone\_lib="Phoma-infected"  
/tissue\_type="leaf"  
/dev\_stage="Pathogen-induced, young trifoliolate"  
/note="Vector: Bluescript SK(-); Young trifoliolate leaves of Medicago truncatula were excised and dip-inoculated in a spore suspension of Phoma medicaginis, and incubated in humid dishes. Pools of leaves were harvested at 0, 15, and 30 minutes and 1, 2, 3, 6, 14, 24, 48, 72, and 96, hours, and used to prepare total RNA. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using ExAssist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOUT cells."

BASE COUNT 188 a 151 c 64 g 224 t 264 others  
ORIGIN

Query Match 52.0%; Score 75.4; DB 14; Length 891;  
Best Local Similarity 87.8%; Pred. No. 7.6e-15;  
Matches 79; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 46 GTGATCCCCGGGCTGAGATTCATATCAAGCTTATGACCTGACCTGAGG 105  
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DB 84 GTGATCCCCGGGCTGAGATTCATATCAAGCTTATGATGATCCGCTGAGG 143  
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QY 106 GGGGGCTTAACCTAATTTGTTTGT 135  
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DB 144 GGGGGCCGCGTATCTATTTTCTATTT 173  
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RESULT 2  
BI306115/c 182 bp mRNA linear EST 20-JUL-2001  
LOCUS  
DEFINITION NL\_3 G09 Drought stress (leaf) Oryza sativa cDNA clone NL\_3\_G09 3', mRNA sequence.  
ACCESSION BI306115  
VERSION BI306115.1 GI:14981437  
KEYWORDS EST.  
SOURCE Oryza sativa.  
ORGANISM Oryza sativa.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretidoideae; Oryzoideae; Oryza.  
1 (bases 1 to 182)  
Reddy A.R., Ramakrishna W., Chandrasekhar A., Nagabushan, I., Ravindrababu, P. and Bennetzen, J. L.  
Novel EST enrichment with normalized cDNA libraries from drought stressed rice (Oryza sativa L. cv Nagina 22)  
Unpublished (2001)  
Contact: Reddy AR  
Department of Plant Sciences, School of Life Sciences  
University of Hyderabad  
P.O. Central university, Hyderabad-500 046, A.P., India  
Tel: 0091-40-3010265  
Fax: 0091-40-3010145  
Email: arjuls@uohyd.ernet.in  
Insert length: 182 Std Error: 0.00  
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Seq primer: GTAAACGACGGCCAGTC.  
Location/Qualifiers  
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/organism="Oryza sativa"

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source

/cultivar="Nagina 22 (indica sub sp.)"  
/db\_xref="taxon:4530"  
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/note="Organ: leaf; Vector: T7T3Pac; ESTs from normalized leaf cDNA library from drought stressed seedlings"  
BASE COUNT 34 a 47 c 53 g 48 t  
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Query Match 49.7%; Score 72; DB 13; Length 182;  
Best Local Similarity 93.8%; Pred. No. 1e-13;  
Matches 75; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 46 GTGATCCCCGGGCTGAGATTCATATCAAGCTTATGACCTGACCTGAGG 105  
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DB 107 GTGATCCCCGGGCTGAGATTCATATCAAGCTTATGATGATCCGCTGAGG 48  
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QY 106 GGGGGCTTAACCTAATTT 125  
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DB 47 GGGGGCCGAGTATCCCAATT 28  
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RESULT 3  
B0143916 793 bp mRNA linear EST 24-APR-2002  
LOCUS  
DEFINITION NF038H04D1F1041 Drought Medicago truncatula cDNA clone NF038H04D 5', mRNA sequence.  
ACCESSION B0143916  
VERSION B0143916.1 GI:20280975  
KEYWORDS EST.  
SOURCE barrel medic.  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.  
1 (bases 1 to 793)  
Torrez-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library  
Unpublished (2000)  
Contact: May GD  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7391  
Fax: 580 221 7380  
Email: gdmay@noble.org  
Insert length: 793 Std Error: 0.00  
Plate: 038 row: H column: 04  
Seq primer: TCACACAGGAACAGCTATGAC.  
Location/Qualifiers  
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FEATURES  
source

BASE COUNT 217 a 203 c 205 g 168 t  
ORIGIN

Query Match 49.7%; Score 72; DB 14; Length 793;  
Best Local Similarity 93.8%; Pred. No. 1.1e-13;  
Matches 75; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 46 GTGATCCCCGGGCTGAGATTCATATCAAGCTTATGATGATCCGCTGAGG 105



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OY	106	GGGGGCTTAATAATT	125	
Dn	145	GGGGGCCGAGTACCATT	164	
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LOCUS	CNS06W11	841 bp	DNA	linear GSS 06-JUL-2001
DEFINITION	T7 end of clone AX0A027B04 of library AX0AA from strain CBS 7064			
ACCESSION	Pichia farinosa, genomic survey sequence.			
VERSION	AL417851			
KEYWORDS	Al417851.1 GI:12200086			
SOURCE	GSS:			
ORGANISM	Pichia farinosa.			
REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
AUTHORS	Saccharomycetales; Saccharomycetaceae; Pichia. 1 (bases 1 to 841) Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bojito-Ekubara,M., Bon,E., Brotier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durans,P., Lepingle,A., Lorente,B., Malpertuy,A., Neugeglise,C., Ozier-Kalogeropoulos,O., Potier,S., Sarrin,W., Tekala,F., Toffano-Nicche,C., Weslowski-Louvel,M., Wincker,P. and Weissbach,J. Genomic exploration of the hemiascomycetous yeasts : 1. A set of yeast species for molecular evolution studies FEMS Lett. 487 (1), 3-12 (2000)			
JOURNAL MEDLINE	20584711			
PUBMED	11152876			
REFERENCE	2 (bases 1 to 841) de Montigny,J., Spehner,C., Souciet,J., Tekala,F., Dujon,B., Wincker,P., Artiguenave,F. and Potier,S. Genomic exploration of the hemiascomycetous yeasts : 15. Pichia sorbitophila FEMS Lett. 487 (1), 87-90 (2000)			
TITLE	20584725			
JOURNAL MEDLINE	11152890			
PUBMED	3 (bases 1 to 841) Genoscope. Direct Submission Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremlieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqlife@genoscope.cns.fr Web : www.genoscope.cns.fr)			
REFERENCE	This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxi, Saccharomycetes kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 tc 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremely of this insert.			
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Query Match	48.6% ; Score 70.4 ; DB 17 ; Length 841 ;			
Best Local Similarity	87.5% ; Pred. No. 3.8e-13 ;			
Matches	77 ; Conservative 0 ; Mismatches 11 ; Indels 0 ; Gaps 0 ;			
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Db	728	TACCTAGACAGACAGAGATGACGAGATGCCCGGGGCTGCAGGAATTCATATCAAGCTTA	787
QY	85	TCGATACCGTCACCTCGAGGGGGGCC	112
CNS06VAH			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
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AUTHORS			
TITLE			
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AUTHORS			
TITLE			
JOURNAL			

QY 95 CGACCTCGAGGGGGGCC 112  
DB 485 CGACCTCGAGGGGGGCC 502

RESULT 6  
LOCUS A0074693/c  
DEFINITION CIT-HSP-2301L23.TF CIT-HSP Homo sapiens genomic clone 2301L23, DNA  
SEQUENCE  
ACCESSION A0074693  
VERSION A0074693.1 GI:3436811  
KEYWORDS GSS.

SOURCE human  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 682)  
Adams,M.D., Rounsley,S.D., Zhao,S., Baas,S., Linher,K., Golden,K.,  
Berry,K., Granger,D., Sub,E., Wible,C., Shizuya,H., Simon,M. and  
Venter,J.C.  
AUTHORS Venter,J.C.  
TITLE Use of a random human BAC End Sequence Database for Sequence-Ready  
Map Building  
JOURNAL Unpublished (1998)  
COMMENT Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: mdadams@tigr.org  
Clones are available from Research Genetics (info@resgen.com). BAC  
end search page:  
http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html.  
Seq primer: M13-21  
Class: BAC ends.

FEATURES  
source Location/Qualifiers  
1..682  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="2301L23"  
/clone\_lib="CIT-HSP"  
/sex="Male"  
/cell\_type="Sperm"  
/note="Vector: pBelobAC1; site\_1: HindIII; site\_2:  
HindIII"

BASE COUNT 156 a 187 c 187 g 151 t 1 others

ORIGIN

Query Match 48.3%; Score 70; DB 17; Length 682;  
Best Local Similarity 93.6%; Pred. No. 5.2e-13;  
Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 46 GTGATATCCCCCGGCTGCGAATTCATATCAAGCTTATGATACCGTGCACCTCGAG 105  
DB 78 GTGATATCCCCCGGCTGCGAATTCATATCAAGCTTATGATACCGTGCACCTCGAG 19

QY 106 GGGGGCCTAACTACTAA 123  
DB 18 GGGGGCCCGAGTACC 1

RESULT 7  
LOCUS B0158468  
DEFINITION B0158468 804 bp mRNA linear EST 24-APR-2002  
clone NF058H09PL1078 Phosphate starved leaf Medicago truncatula CDNA  
ACCESSION B0158468  
VERSION B0158468.1 GI:20295525  
KEYWORDS EST.  
SOURCE barrel medic.  
ORGANISM Medicago truncatula

REFERENCE 1 (bases 1 to 804)  
AUTHORS Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores  
H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.  
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
JOURNAL Medicago truncatula phosphate-starved leaf library  
COMMENT Unpublished (2000)  
Contact: Harrison MJ  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7325  
Fax: 580 221 7380  
Email: mjharrison@noble.org  
Insert Length: 804 Std Error: 0.00  
Plate: 058 row: H column: 09  
Seq primer: TCACACAGGAACACCTATGAC.

FEATURES  
source Location/Qualifiers  
1..804  
/organism="Medicago truncatula"  
/db\_xref="taxon:3880"  
/clone="NF058H09PL"  
/clone\_lib="phosphate starved leaf"  
/tissue\_type="leaf"  
/dev\_stage="trifoliolate"  
/note="Vector: Lambda Zap; At the trifoliolate stage, M.  
truncatula plants were transplanted to phosphate-free sand  
and grown for a further 30 days. During this 30 day  
period, the plants were fertilized twice weekly with 1/2  
Hoaglands solution containing only 20mM potassium  
phosphate. RNA was prepared from above ground tissues."

BASE COUNT 215 a 202 c 181 g 165 t 41 others

ORIGIN

Query Match 48.1%; Score 69.8; DB 14; Length 804;  
Best Local Similarity 89.2%; Pred. No. 6.1e-13;  
Matches 74; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 46 GTGATATCCCCCGGCTGCGAATTCATATCAAGCTTATGATACCGTGCACCTCGAG 105  
DB 82 GTGATATCCCCCGGCTGCGAATTCATATCAAGCTTATGATACCGTGCACCTCGAG 141

QY 106 GGGGGCCTAACTACTATTG 128  
DB 142 GGGGGCCTGTRACCAATTC 164

RESULT 8  
LOCUS CNS06XBT  
DEFINITION CNS06XBT 355 bp DNA linear GSS 06-JUN-2001  
T7 end of clone XAX0A001B07 of library XAX0A from strain CBS 7064  
of Pichia farinosa, genomic survey sequence.  
ACCESSION AL419535  
VERSION AL419535.1 GI:12202713  
KEYWORDS GSS.  
SOURCE Pichia farinosa.  
ORGANISM Pichia farinosa.  
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; Saccharomycetaceae; Pichia.  
REFERENCE 1 (bases 1 to 355)  
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,  
Boulotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,  
de-Montigny,J., Dujon,B., Durans,P., Lepingle,A., Lorente,B.,  
Malpertuy,A., Neuvéglise,C., Ozier-Kalogiropoulos,O., Potier,S.,  
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,  
Wincker,P. and Weissbach,J.  
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of  
yeast species for molecular evolution studies  
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)  
MEDLINE 20584711

PUBMED 11152876  
 REFERENCE 2 (bases 1 to 355)  
 AUTHORS de Montigny,J., Spehner,C., Souciet,J., Tekala,F., Dujon,B., Winkler,P., Artiguenave,F. and Potier,S.  
 TITLE Genomic exploration of the hemiascomycetous yeasts: 15. *Pichia sorbitophila*  
 JOURNAL FEBS Lett. 487 (1), 87-90 (2000)  
 MEDLINE 20584725  
 PUBMED 11152890  
 REFERENCE 3 (bases 1 to 355)  
 AUTHORS Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
 COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvaurum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.  
 FEATURES  
 Source  
 1. 355  
 /organism="Pichia farinosa"  
 /strain="CBS 7064"  
 /db\_xref="taxon:4920"  
 /clone="XAX0A001B07"  
 /clone\_1lb="XAX0A"  
 /note="end : T7"  
 BASE COUNT 64 a 91 c 109 g 86 t 5 others  
 ORIGIN  
 Query Match 48.0%; Score 69.6; DB 17; Length 355;  
 Best Local Similarity 92.3%; Pred. No. 6.9e-13;  
 Matches 72; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 35 ACGGCGCCCGTGGATGCCCGGGGCTGCAGAAATGCAATCAAGCTTATCATACCGT 94  
 Db 242 ACTCGGCGGCTGCTGATGCCCGGGGCTGCAGAAATGCAATCAAGCTTATCATACCGT 301  
 QY 95 CGACCTCGAGGGGGGCC 112  
 Db 302 CGACCTCGAGGGGGGCC 319  
 RESULT 9  
 BI305962/c  
 LOCUS NL\_2\_K23 Drought stress (leaf) Oryza sativa cDNA clone NL\_2\_K23 3', mRNA  
 DEFINITION NL\_2\_K23 Drought stress (leaf) Oryza sativa cDNA clone NL\_2\_K23 3', mRNA sequence.  
 ACCESSION BI305962  
 VERSION BI305962.1 GI:14981284  
 KEYWORDS EST.  
 SOURCE Oryza sativa.  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 182)  
 AUTHORS Reddy,A.R., Ramakrishna,W., Chandrasekhar,A., Nagabhusan,I., Ravindrababu,P. and Bennetzen,J.L.  
 TITLE Novel EST enrichment with normalized cDNA libraries from drought stressed rice (Oryza sativa L.cv Nagina 22)  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Reddy AR  
 Department of Plant Sciences, School of Life Sciences  
 University of Hyderabad  
 P.O. Central University, Hyderabad-500 046, A.P., India  
 Tel: 0091-40-3010265

Fax: 0091-40-3010145  
 Email: arjuls@uohyd.ernet.in  
 Insert Length: 182 Std Error: 0.00  
 Plate: 2 row: K column: 23  
 Seq primer: GTAAACGACGCGCAGTG.  
 FEATURES  
 Source  
 1. 182  
 /organism="Oryza sativa"  
 /cultivar="Nagina 22 (indica sub sp)"  
 /db\_xref="taxon:4530"  
 /clone="NL\_2\_K23"  
 /clone\_1lb="Drought stress (leaf)"  
 /tissue\_type="Entire leaf tissue"  
 /dev\_stage="35 day-old seedlings"  
 /note="Organ: Leaf; Vector: T773Pac; ESTs from normalized leaf cDNA library from drought stressed seedlings"  
 BASE COUNT 34 a 48 c 52 g 46 t 2 others  
 ORIGIN  
 Query Match 47.9%; Score 69.4; DB 13; Length 182;  
 Best Local Similarity 91.2%; Pred. No. 7.9e-13;  
 Matches 73; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 46 GTGATCCCCCGGCTGCAGAAATGCAATCAAGCTTATCATACCGTGCAGCTGAGG 105  
 Db 107 GTGATCCCCCGGCTGCAGAAATGCAATCAAGCTTATCATACCGTGCAGCTGAGG 48  
 QY 106 GGGGCGCTAATCAATAT 125  
 Db 47 GGGGCGCGGTACCAAT 28  
 RESULT 10  
 BI305695/c  
 LOCUS NL\_1\_G23 Drought stress (leaf) Oryza sativa cDNA clone NL\_1\_G23 3', mRNA  
 DEFINITION NL\_1\_G23 Drought stress (leaf) Oryza sativa cDNA clone NL\_1\_G23 3', mRNA sequence.  
 ACCESSION BI305695  
 VERSION BI305695.1 GI:14981017  
 KEYWORDS EST.  
 SOURCE Oryza sativa.  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 186)  
 AUTHORS Reddy,A.R., Ramakrishna,W., Chandrasekhar,A., Nagabhusan,I., Ravindrababu,P. and Bennetzen,J.L.  
 TITLE Novel EST enrichment with normalized cDNA libraries from drought stressed rice (Oryza sativa L.cv Nagina 22)  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Reddy AR  
 Department of Plant Sciences, School of Life Sciences  
 University of Hyderabad  
 P.O. Central University, Hyderabad-500 046, A.P., India  
 Tel: 0091-40-3010265  
 Fax: 0091-40-3010145  
 Email: arjuls@uohyd.ernet.in  
 Insert Length: 186 Std Error: 0.00  
 Plate: 1 row: G column: 23  
 Seq primer: GTAAACGACGCGCAGTG.  
 FEATURES  
 Source  
 1. 186  
 /organism="Oryza sativa"  
 /cultivar="Nagina 22 (indica sub sp)"  
 /db\_xref="taxon:4530"  
 /clone="NL\_1\_G23"  
 /clone\_1lb="Drought stress (leaf)"  
 /tissue\_type="Entire leaf tissue"  
 /dev\_stage="35 day-old seedlings"  
 /note="Organ: Leaf; Vector: T773Pac; ESTs from normalized leaf cDNA library from drought stressed seedlings"  
 BASE COUNT 35 a 47 c 56 g 46 t 2 others

ORIGIN

Query Match 47.9%; Score 69.4; DB 13; Length 186;  
 Best Local Similarity 91.2%; Pred. No. 7.9e-13;  
 Matches 73; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 46 GTGATCCCGGGGCTGAGAAATTCGATTCAGCTTATCGATTACCGTCGACCTGAGG 105  
 |||  
 DB 111 GTGATCCCGGGGCTGAGAAATTCGATTCAGCTTATCGATTACCGTCGACCTGAGG 52  
 |||

QY 106 GGGGCTACTACTAATTT 125  
 |||  
 DB 51 GGGGGCNCGGTACCCCAATT 32  
 |||

RESULT 11  
 BH001110

LOCUS 574 bp DNA linear GSS 01-JUL-2001

DEFINITION G139 Gemmata obscuriglobus phagemid library Gemmata obscuriglobus genomic clone G139 similar to cadmium efflux system accessory protein, DNA sequence.

ACCESSION BH001110 GI:14579876

KEYWORDS GSS.

SOURCE Gemmata obscuriglobus.

ORGANISM Gemmata obscuriglobus  
 Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;  
 Planctomycetaceae; Gemmata.  
 1 (bases 1 to 574)

REFERENCE  
 AUTHORS Jenkins,C., Kedar,V. and Fuerst,J.A.  
 TITLE Gene discovery from sequence tags generated using genomic DNA libraries constructed from representatives of the planctomycete division of the Domain Bacteria  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Fuerst JA  
 Department of Microbiology and Parasitology  
 University of Queensland  
 Brisbane, QLD 4072, Australia  
 Tel: +617 3365 4643  
 Fax: +617 3365 4620  
 Email: fuerst@biosci.uq.edu.au  
 Class: shotgun.

FEATURES  
 source  
 Location/Qualifiers  
 1..574  
 /organism="Gemmata obscuriglobus"  
 /strain="ACM 2246"  
 /db\_xref="taxon:114"  
 /clone="G139"  
 /clone\_lib="Gemmata obscuriglobus phagemid library"  
 /lab\_host="Escherichia coli strain XL1-Blue"  
 /note="Vector: pBluescript II SK(-) phagemid; Site 1: BamHI; Site 2: BamHI; Purified genomic DNA from Gemmata obscuriglobus was restricted with Sau3AI to give fragments of 400-3000bp and ligated into the BamHI site of the pBluescript II SK(-) phagemid. The ligated DNA was electroporated into E. coli XL1-Blue."

BASE COUNT 117 a 161 c 163 g 130 t 3 others

ORIGIN

Query Match 47.7%; Score 69.2; DB 17; Length 574;  
 Best Local Similarity 90.2%; Pred. No. 9.6e-13;  
 Matches 74; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 31 TTGACGCGCGCGCGATGCCCGGCTGAGAAATTCGATTCAGCTTATCGATA 90  
 |||  
 DB 408 TTGACGCGCTACTGTGTTATCCCGGCTGAGAAATTCGATTCAGCTTATCGATA 467  
 |||

QY 91 CCGTCGACTCGAGGGGGGCC 112  
 |||  
 DB 468 CCGTCGACTCGAGGGGGGCC 489  
 |||

RESULT 12

CNS06UF5

LOCUS 912 bp DNA linear GSS 06-JUL-2001

DEFINITION T7 end of clone AX0AA008E09 of library AX0AA from strain CBS 7064 of Pichia farinosa, genomic survey sequence.

ACCESSION ALA15767

VERSION ALA15767.1 GI:12195405

KEYWORDS GSS.

SOURCE Pichia farinosa.

ORGANISM Pichia farinosa  
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 Saccharomycetales; Saccharomycetaceae; Pichia.  
 1 (bases 1 to 912)

REFERENCE  
 AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.  
 TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies  
 JOURNAL FEMS Lett. 487 (1), 3-12 (2000)  
 MEDLINE 20584711  
 PUBMED 11152876

REFERENCE  
 AUTHORS 2 (bases 1 to 912)  
 de Montigny,J., Spennet,C., Souciet,J., Tekala,F., Dujon,B., Wincker,P., Artiguenave,F. and Potier,S.  
 TITLE Genomic exploration of the hemiascomycetous yeasts: 15. Pichia sorbitophila  
 FEMS Lett. 487 (1), 87-90 (2000)  
 MEDLINE 20584725  
 PUBMED 11152890

REFERENCE  
 AUTHORS 3 (bases 1 to 912)  
 Direct Submission  
 Submitted (07-SEP-2000) Genoscope - Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seque@genoscope.cns.fr - Web: www.genoscope.cns.fr)  
 TITLE This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES  
 source  
 Location/Qualifiers  
 1..912  
 /organism="Pichia farinosa"  
 /strain="CBS 7064"  
 /db\_xref="taxon:4920"  
 /clone="AX0AA008E09"  
 /clone\_lib="AX0AA"  
 /note="End: 177"

BASE COUNT 298 a 210 c 160 g 240 t 4 others

ORIGIN

Query Match 47.7%; Score 69.2; DB 17; Length 912;  
 Best Local Similarity 88.1%; Pred. No. 9.8e-13;  
 Matches 74; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 47 TGGATCCCGCGGGCTGAGAAATTCGATTCAGCTTATCGATACCGTCGAGAGG 106  
 |||  
 DB 817 TGGATCCCGCGGGCTGAGAAATTCGATTCAGCTTATCGATACCGTCGAGAGG 876  
 |||

QY 107 GGGGCTACTACTAATTTGTT 130  
 |||  
 DB 877 GGGGCTACTACTAATTTGTT 900  
 |||

RESULT 13  
 BE428068

LOCUS BE428068 162 bp mRNA linear EST 26-JUL-2000  
 DEFINITION MTD002.H10F990615 ITEC MTD Durum Root Library Triticum  
 turgidum subsp. durum cDNA clone MTD002.H10, mRNA sequence.  
 ACCESSION BE428068  
 VERSION BE428068.1 GI:9425911  
 KEYWORDS EST.  
 SOURCE durum wheat.  
 ORGANISM Triticum turgidum subsp. durum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae  
 ; Triticaceae; Triticum.  
 1 (bases 1 to 162)  
 REFERENCE  
 AUTHORS Anderson O.A., Appels R., Bailey P., Blake T., Close T., Cloutier  
 S., Dubcovsky J., Feuillet C., Gale M., Graner A., Gustafson P.,  
 Herrmann R.G., Holton T., Jacquemin J.M., Jia J., Joudrier P.,  
 Langridge P., Izzo G.R., Lin J.J., McGuire P., Ogihara Y.,  
 Perchionni N., Qualset C., Schuch W., Selvaraj G., Shariflou M.,  
 Sorrells M., Warburton M. and Wenzel G.  
 International Triticaceae EST Cooperative (ITEC): Production of  
 International Triticaceae EST Cooperative (ITEC): Production of  
 Expressed Sequence Tags for Species of the Triticaceae  
 Unpublished (2000)  
 CONTACT: Joudrier P  
 JINRA, Unite de Biochimie et Biologie Molculaire des Cereales  
 2, place VIALA, 34060 Montpellier cedex 01 FRANCE  
 Tel: 33 4 99 61 23 84  
 Fax: 33 4 99 61 23 84  
 Email: joudrier@enscm.jnra.fr  
 International Triticaceae EST Cooperative (ITEC)  
 http://wheat.pw.usda.gov/genome.  
 FEATURES  
 source  
 1..162  
 /organism="Triticum turgidum subsp. durum"  
 /cultivar="Silihana"  
 /db\_xref="taxon:4567"  
 /clone="MTD002.H10"  
 /clone\_lib="ITEC MTD Durum Wheat Root Library"  
 /tissue\_type="root"  
 /dev\_stage="3-day-old seedling, water-stressed"  
 /note="Vector: pSPORT1; T7 primers used. See pSPORT1  
 polylinker site. 0.3-2.0 kbp average insert size."  
 BASE COUNT 28 a 42 c 49 g 43 t  
 ORIGIN  
 Query Match 47.6%; Score 69; DB 10; Length 162;  
 Best Local Similarity 88.2%; Pred. No. 1.1e-12;  
 Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 46 GTGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGCTCGAGG 105  
 |||||||  
 DB 24 GTGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGCTCGAGG 83  
 |||||||  
 QY 106 GGGGCGCTACACTAATTTGTT 130  
 |||||||  
 DB 84 GGGGCGCGGTACCAAGCTTTGTT 108  
 |||||||  
 RESULT 14  
 LOCUS AU234451 390 bp mRNA linear EST 21-SEP-2001  
 DEFINITION AU234451 Bovine placenta cDNA Bos taurus cDNA Cln1153 3',  
 mRNA sequence.  
 ACCESSION AU234451  
 VERSION AU234451.1 GI:15719669  
 KEYWORDS EST.  
 SOURCE cow.  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.  
 REFERENCE  
 AUTHORS Gohma H., Lejuko H.Y., Taniguchi Y., Yamada T., Akagi S., Yasue  
 H. and Sasaki Y.  
 Analysis of expressed sequence tags from a cDNA library of bovine

JOURNAL placenta  
 COMMENT Unpublished (2001)  
 Contact: Takahisa Yamada  
 Graduate School of Agriculture  
 Kyoto University  
 Sakyo-ku, Kitashirakawa, Kyoto, Kyoto 606-8502, Japan  
 Tel: 81-75-753-6323  
 Fax: 81-75-753-6340  
 Email: tyamada@kans.jkns.kais.kyoto-u.ac.jp  
 This clone was obtained from a 3' end cDNA library.  
 FEATURES  
 source  
 1..390  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone="Cln1153"  
 /clone\_lib="Bovine placenta cDNA"  
 /tissue\_type="placenta"  
 /note="Vector: pUC18 Sma I/BAP"  
 BASE COUNT 113 a 77 c 128 t  
 ORIGIN  
 Query Match 47.6%; Score 69; DB 9; Length 390;  
 Best Local Similarity 88.2%; Pred. No. 1.1e-12;  
 Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 46 GTGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGCTCGAGG 105  
 |||||||  
 DB 300 GTGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGCTCGAGG 359  
 |||||||  
 QY 106 GGGGCGCTACACTAATTTGTT 130  
 |||||||  
 DB 360 GGGGCGCGGTACCAAGCTTTGTT 384  
 |||||||  
 RESULT 15  
 LOCUS AU278852/c 400 bp mRNA linear EST 02-JUL-2002  
 DEFINITION AU278852 Cloned bovine placenta cDNA Bos taurus cDNA clone  
 placental1153 3', mRNA sequence.  
 ACCESSION AU278852  
 VERSION AU278852.1 GI:21682162  
 KEYWORDS EST.  
 SOURCE cow.  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.  
 REFERENCE  
 AUTHORS Oishi M., Yamada T., Goma H., Lejuko H.Y., Taniguchi Y. and  
 Sasaki Y.  
 EST analysis of cloned bovine fetus and placenta  
 Unpublished (2002)  
 Contact: Masahito Oishi  
 Graduate School of Agriculture  
 Kyoto University  
 Sakyo-ku, Kitashirakawa, Kyoto, Kyoto 606-8502, Japan  
 Tel: 81-75-753-6331  
 Fax: 81-75-753-6340  
 Email: oishi@kans.jkns.kais.kyoto-u.ac.jp.  
 FEATURES  
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 1..400  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone="placental1153"  
 /clone\_lib="Cloned bovine placenta cDNA"  
 /dev\_stage="60 embryonic day"  
 /note="Organ: ovary; Vector: pGEM-T Easy; Randomly cloned  
 third differential products (Dp3) of a Representational  
 Differential Analysis (RDA) with bovine corpus luteum as  
 tester tissue and skeletal muscle as driver."  
 BASE COUNT 133 a 73 c 79 g 115 t  
 ORIGIN

Query Match 47.6%; Score 69; DB 9; Length 400;  
Best Local Similarity 88.2%; Pred. No. 1.1e-12;  
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 46 GTGATCCCCCGGCGTGCAGGAAATTCGATATCAAGCTTATCGATACGCTCGACCTCGAGG 105  
DB 91 GTGATCCCCCGGCGTGCAGGAAATTCGATATCAAGCTTATCGATACGCTCGACCTCGAGG 32  
QY 106 GGGGCTTACTTACTTAAATTTGTT 130  
DB 31 GGGGCGCGGTACCCAGCTTTGTT 7

Search completed: November 10, 2002, 08:33:09  
Job time : 1310 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 04:19:15 ; Search time 171.087 Seconds  
(without alignments)  
1908.619 Million cell updates/sec

Title: US-08-935-377-6

Sequence: 1 GGCCAAATGTAATACTA.....TTGTTTGTGGCCGCCGCC 145

Scoring table: IDENTITY\_NUC  
Gap 10.0 , Capext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:\*  
24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145	100.0	145	21	AAA15235
2	145	100.0	145	22	ABA01476
3	145	100.0	145	24	AAD31778
4	132	91.0	148	21	AAA15236
5	132	91.0	148	22	ABA01477
6	132	91.0	148	24	AAD31779
7	131	90.3	149	21	AAA15237
8	131	90.3	149	22	ABA01478
9	131	90.3	149	24	AAD31780

10	130	89.7	150	21	AAA15238	Nucleotide sequence
11	130	89.7	150	22	ABA01479	Partial p7.5/ATG3/
12	130	89.7	150	24	AAD31781	Modified p7.5/tk v
13	71.6	49.4	460	23	ABV33323	Human prostate exp
14	71.6	49.4	460	23	ABV43246	Human prostate exp
15	70.8	48.8	508	23	ABV39281	Human prostate exp
16	70.6	48.7	333	23	ABV45519	Human prostate exp
17	70.6	48.7	392	23	ABV38605	Human prostate exp
18	70.6	48.7	455	23	ABV31882	Human prostate exp
19	70.6	48.7	459	23	ABV35787	Human prostate exp
20	70.6	48.7	552	23	ABV44587	Human prostate exp
21	70.6	48.7	552	23	ABV35639	Human prostate exp
22	70.6	48.7	659	23	ABV39144	Human prostate exp
23	70.6	48.7	659	23	ABV45482	Human prostate exp
24	70.6	48.7	659	23	ABV45486	Human prostate exp
25	70.4	48.6	276	23	ABV35118	Human prostate exp
26	70.4	48.6	375	23	ABV44301	Human prostate exp
27	70.4	48.6	5592	24	AAD35631	Plasmid pTV05 full
28	70.2	48.4	5804	24	ABA96439	Plasmid pSV05 SEO
29	70	48.3	377	23	ABV37034	Human prostate exp
30	70	48.3	400	23	ABV33919	Human prostate exp
31	70	48.3	400	23	ABV42794	Human prostate exp
32	70	48.3	439	23	ABV38640	Human prostate exp
33	70	48.3	567	23	ABV31904	Human prostate exp
34	70	48.3	567	23	ABV40860	Human prostate exp
35	70	48.3	626	23	ABV34271	Human prostate exp
36	70	48.3	630	23	ABV35248	Human prostate exp
37	69.6	48.0	505	23	ABV33645	Human prostate exp
38	69.6	48.0	505	23	ABV42560	Human prostate exp
39	69.4	47.9	411	23	ABV36341	Human prostate exp
40	69.4	47.9	411	23	ABV45372	Human prostate exp
41	69.4	47.9	916	24	AA146542	E gossypii coding
42	69.4	47.9	13558	22	AA166274	Murine apoptase L1
43	69.2	47.7	437	23	ABV38437	Human prostate exp
44	69	47.6	184	23	ABV35188	Human prostate exp
45	69	47.6	205	23	ABV31861	Human prostate exp

#### ALIGNMENTS

RESULT 1	
AAA15235	AAA15235 standard; DNA; 145 BP.
XX	
AC	AAA15235:
XX	
DT	04-SEP-2000 (first entry)
XX	
DE	Nucleotide sequence of a fragment of the plasmid p7.5/ATG0/tk.
XX	
KW	Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;
KM	vaccine; tumour regression; cancer; infection; ss.
XX	
OS	Synthetic.
XX	
PN	WO200028016-A1.
XX	
PD	18-MAY-2000.
XX	
PF	10-NOV-1998; 98WO-US24029.
XX	
PR	10-NOV-1998; 98WO-US24029.
XX	
PA	(UYRP ) UNIV ROCHESTER.
XX	
PI	Zauderer M;
XX	
DR	WPI; 2000-376533/32.
XX	
PT	Novel method of identifying target epitopes or antigens specific for
PT	human tumors, cancers and infected cells involving screening expression
PT	library products of a cell expressing the target epitope

xx	Disclosure: Fig 2; 132pp; English.
ps	
xx	
cc	The present sequence represents a fragment of a vaccinia transfer
cc	plasmid, which is used in the course of the invention. The
cc	specification describes a method for identifying a target epitope.
cc	The method comprises screening the products of an expression library
cc	from a cell expressing the target epitope with cytotoxic T cells
cc	generated against the cell to identify DNA clones expressing the target
cc	epitope. The method may also comprise providing a cytotoxic T cell
cc	specific for a gene product differentially expressed by a cell and
cc	measuring the cross-reactivity of the cytotoxic T cell. The methods are
cc	useful for identifying tumour specific target epitopes and antigens which
cc	are useful in immunogenic compositions or vaccines to induce the
cc	regression of tumors, cancers or infections in mammals. The genes
cc	expressed in a panel of tumour cells that are derived from single
cc	immortalised, non-tumourigenic cell line are used to generate HLA
cc	restricted cytotoxic T cells which are evaluated for activity against
cc	tumour cells. The method is useful to identify potential antigens
cc	expressed not only by the pathogen but also by the host cells whose gene
cc	expression is altered as a result of infection. The differential gene
cc	expression strategies can be applied to identify immunogenic molecules
cc	of cells infected with virus, fungus or mycobacterium.
xx	
xx	
so	Sequence 145 BP; 34 A; 37 C; 38 G; 36 T; 0 other;
	Query Match 100.0%; Score 145; DB 21; Length 145;
	Best Local Similarity 100.0%; Pred. No. 2,1e-40;
	Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 GGGCAAAATTGAANAAGTATGATCTATTATTATGACACGGCGCGGTGATCCCCGGGC 60
Db	1 GGGCAAAATTGAANAAGTATGATCTATTATTATGACACGGCGCGGTGATCCCCGGGC 60
OY	61 TGCAGAAATTCATATTCAGCTTATTCGATACCGGTGACCTCGAGGGGGGCGCTAACTAAC 120
Db	61 TGCAGAAATTCATATTCAGCTTATTCGATACCGGTGACCTCGAGGGGGGCGCTAACTAAC 120
OY	121 TAATTTTGTTTTGTGGGGCCGGCC 145
Db	121 TAATTTTGTTTTGTGGGGCCGGCC 145
	RESULT 2
	ABA01476
ID	ABA01476 standard; DNA; 145 BP.
xx	
AC	ABA01476;
xx	
DT	04-FEB-2002 (first entry)
xx	
DE	Partial p7.5/ATG0/tk sequence.
xx	
KM	Cell death; toxic gene; tumour suppressor; ds.
OS	Synthetic.
xx	
PN	WO200172995-A2.
xx	
PD	04-OCT-2001.
xx	
PF	28-MAR-2001; 2001WO-US09953.
xx	
PR	28-MAR-2000; 2000US-0192586.
PR	10-MAY-2000; 2000US-0203343.
PR	23-JAN-2001; 2001US-0263226.
xx	
PR	27-FEB-2001; 2001US-0271426.
xx	
PA	(UNYP ) UNIV ROCHESTER.
xx	
PI	Zauderer M, Smith ES;
xx	
DR	WPI; 2001-570897/64.
xx	

XX	Selecting target polynucleotides, particularly toxic genes, involves
PT	introducing a library of insert polynucleotides into a host cell
PT	population, where the target polynucleotide promotes cell death -
XX	
P5	Disclosure; Fig 8; 359pp; English.
XX	
CC	The present invention relates to a method for selecting a target
CC	polynucleotide. The method comprises introducing into a host cell
CC	a population a library of insert polynucleotides, where expression of the
CC	target polynucleotide directly or indirectly promotes host cell death.
CC	The cells are cultured and the insert polynucleotides are collected from
CC	the cells which die. The method is useful for selecting target
CC	polynucleotides, particularly polynucleotides which alter cell phenotypes
CC	of induce or inhibit cell death. The method can be used to isolate toxic
CC	genes such as tumour suppressors. The present sequence was used to
CC	illustrate the method of the present invention.
XX	
SQ	Sequence 145 BP; 34 A; 37 C; 38 G; 36 T; 0 other;
Query Match	100.0%; Score 145; DB 22; Length 145;
Best Local Similarity	100.0%; Pred No. 2,1e+40;
Matches 145; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	1 GGCCAAAATTGAAAACTAGATCTATTATTTCACGGCGCCGCGTGATCCCCGGGC 60
DB	1 GCCCAAAATFGAAAACTAGATCTATTATTTCACGGCGCCGCGTGATCCCCGGGC 60
OY	61 TGCGAGATTGGAATACGTATCATGATCGCTGCACCTCGAAGGGGGGGCCTACTAAC 120
DB	61 TGCGAGATTGGAATACGTATCATGATCGCTGCACCTCGAAGGGGGGGCCTACTAAC 120
OY	121 TAATTTGTTTTTGTGGGCCCGCC 145
DB	121 TAATTTGTTTTTGTGGGCCCGCC 145
RESULT 3	
AAD31778	ID AAD31778 standard; DNA; 145 BP.
XX	AAD31778;
XX	18-JUN-2002 (first entry)
DE	Modified p7.5/tk vector, p7.5/ATG0/tk.
XX	
KW	Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity.
KM	vaccine; immune response; cyostatic; p7.5/tk vector; thymidine kinase;
KW	p7.5/ATG0/tk vector; ds.
OS	Vaccinia virus.
OS	Synthetic.
XX	
FT	Key Location/Qualifiers
FT	misc_signal 113..115
FT	/tag= a
FT	/note= "translation stop codon"
FT	117..119
FT	/tag= b
FT	/note= "translation stop codon"
FT	121..123
FT	/tag= c
FT	/note= "translation stop codon"
FT	129..135
FT	/tag= d
FT	/note= "transcription stop signal"
XX	
PN	US2002018785-A1.
XX	
PD	14-FEB-2002.
PF	02-APR-2001; 2001US-0822250.



```
XX 22-SEP-1997; 97US-0935377.
XX (UYRP ) UNIV ROCHESTER.
XX Zauderer M;
XX WPI; 2002-239252/29.
XX
XX Representational Difference Analysis method for identification of
XX antigens recognized by cytotoxic T cells and specific for human tumors,
XX comprises improved selection of genes encoding target antigens -
XX
XX Example 1; Fig 2; 54pp; English.
XX
XX The present invention relates to novel methods for the identification
XX of antigens recognised by cytotoxic T cells (CTLs) and specific for
XX human tumours, cancers and infected cells. The method involves screening
XX the products of an expression library generated from DNA/RNA of a cell
XX expressing a target epitope with cytotoxic T cells generated against
XX the cell to identify DNA clones expressing target epitope or providing
XX cytotoxic T cells specific for a gene product differentially expressed
XX by a cell and measuring the cross-reactivity of the cytotoxic T cells
XX for cells expressing a target epitope in which the target epitope is
XX identified as a gene product inducing cytotoxic T cells. The method is
XX useful for identifying a target epitope or antigen specific for a tumour
XX cell. The target epitope is also useful for identifying target antigens
XX in other target cells against which it is desirable to induce cell-
XX mediated immunity. The antigen identified by the method is useful
XX in immunogenic compositions and vaccine preparations to induce the
XX regression of tumours, cancers and infections in mammals. The invention
XX also relates to vaccinia viral vectors which are useful for treating
XX tumour-bearing mammals, including humans to generate immune response
XX against the tumour cells. They are also useful for immunising or
XX vaccinating tumour-free subjects to prevent tumour formation. The
XX present sequence is modified p7.5/tk (thymidine kinase) vector.
XX p7.5/ATG0/tk. This vector comprises a vaccinia virus 7.5K promoter and
XX a modified tk DNA fragment. This vector is used in the exemplification
XX of the invention.
XX
XX Sequence 145 BP; 34 A; 37 C; 38 G; 36 T; 0 other;
XX
XX Query Match 100.0%; Score 145; DB 24; Length 145;
XX Best Local Similarity 100.0%; Pred. No. 2.1e-40;
XX Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGCCTAAATTTGAAAACTAGATCTATTATTGACGCGCGCGCGTGCATCCCGGGC 60
XX |
XX 1 GGCCTAAATTTGAAAACTAGATCTATTATTGACGCGCGCGCGTGCATCCCGGGC 60
XX
XX QY 61 TGCAGGAATTCGATATACACTTATGATACCGTCGACCTCGAGGGGGGCGCTTAAC 120
XX |
XX 61 TGCAGGAATTCGATATACACTTATGATACCGTCGACCTCGAGGGGGGCGCTTAAC 120
XX
XX QY 121 TAATTTGTTTGTGGGCGCGGC 145
XX |
XX 121 TAATTTGTTTGTGGGCGCGGC 145
XX
XX Db 121 TAATTTGTTTGTGGGCGCGGC 145
XX
XX
XX RESULT 4
XX AAA15236
XX ID AAA15236 standard; DNA; 148 BP.
XX
XX AC AAA15236;
XX
XX DT 04-SEP-2000 (first entry)
XX
XX DE Nucleotide sequence of a fragment of the plasmid p7.5/ATG1/tk.
XX
XX KM Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;
XX vaccine; tumour regression; cancer; infection; ss.
XX
XX OS Synthetic.
```

```
XX WO200028016-A1.
XX
XX 18-MAY-2000.
XX
XX 10-NOV-1998; 98WO-US24029.
XX
XX 10-NOV-1998; 98WO-US24029;
XX
XX (UYRP ) UNIV ROCHESTER.
XX Zauderer M;
XX WPI; 2000-376533/32.
XX
XX Novel method of identifying target epitopes or antigens specific for
XX human tumors, cancers and infected cells involving screening expression
XX library products of a cell expressing the target epitope -
XX
XX Disclosure; Fig 2; 132pp; English.
XX
XX The present sequence represents a fragment of a vaccinia transfer
XX plasmid, which is used in the course of the invention. The
XX specification describes a method for identifying a target epitope.
XX The method comprises screening the products of an expression library
XX from a cell expressing the target epitope with cytotoxic T cells
XX generated against the cell to identify DNA clones expressing the target
XX epitope. The method may also comprise providing a cytotoxic T cell
XX specific for a gene product differentially expressed by a cell and
XX measuring the cross-reactivity of the cytotoxic T cell. The methods are
XX useful for identifying tumour specific target epitopes and antigens which
XX are useful in immunogenic compositions or vaccines to induce the
XX regression of tumours, cancers or infections in mammals. The genes
XX expressed in a panel of tumour cells that are derived from single
XX immortalised, non-tumourigenic cell line are used to generate HLA
XX restricted cytotoxic T cells which are evaluated for activity against
XX tumour cells. The method is useful to identify potential antigens
XX expressed not only by the pathogen but also by the host cells whose gene
XX expression is altered as a result of infection. The differential gene
XX expression strategies can be applied to identify immunogenic molecules
XX of cells infected with virus, fungus or mycobacterium.
XX
XX Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;
XX
XX Query Match 91.0%; Score 132; DB 21; Length 148;
XX Best Local Similarity 98.0%; Pred. No. 6.6e-36;
XX Matches 145; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
XX
XX QY 1 GGCCTAAATTTGAAAACTAGATCTATTATTGACGCGCGCGCGTGCATCCCGG 57
XX |
XX 1 GGCCTAAATTTGAAAACTAGATCTATTATTGACGCGCGCGCGTGCATCCCGG 60
XX
XX Db 58 GCGTCGAGGAATTCGATATACAGCTTATGATACCGTCGACCTCGAGGGGGGCGCTTA 117
XX |
XX 61 GCGTCGAGGAATTCGATATACAGCTTATGATACCGTCGACCTCGAGGGGGGCGCTTA 120
XX
XX QY 118 AACTAATTTTGTGTTTGTGGGCGCGGC 145
XX |
XX 121 AACTAATTTTGTGTTTGTGGGCGCGGC 148
XX
XX Db 121 AACTAATTTTGTGTTTGTGGGCGCGGC 148
XX
XX
XX RESULT 5
XX ABA01477
XX ID ABA01477 standard; DNA; 148 BP.
XX
XX AC ABA01477;
XX
XX DT 04-FEB-2002 (first entry)
XX
XX DE Partial p7.5/ATG1/tk sequence.
XX
XX KM Cell death; toxic gene; tumour suppressor; ds.
XX
XX OS
```

OS	Synthetic.
XX	
PN	WO200172995-A2.
PD	
XX	
FD	04-OCT-2001.
XX	
PF	28-MAR-2001; 2001WO-US09953.
XX	
PR	28-MAR-2000; 2000US-0192586.
FR	10-MAY-2000; 2000US-0203343.
PR	23-JAN-2001; 2001US-0263226.
PR	27-FEB-2001; 2001US-0271426.
XX	
PA	(UYRP ) UNIV ROCHESTER.
XX	
PI	Zauderer M, Smith ES;
DR	WPI; 2001-570897/64.
XX	
PT	Selecting target polynucleotides, particularly toxic genes, involves introducing a library of insert polynucleotides into a host cell population, where the target polynucleotide promotes cell death -
PS	Disclosure; Fig 8; 359pp; English.
XX	
CC	The present invention relates to a method for selecting a target polynucleotide. The method comprises introducing into a host cell population a library of insert polynucleotides, where expression of the target polynucleotide directly or indirectly promotes host cell death. The cells are cultured and the insert polynucleotides are collected from the cells which die. The method is useful for selecting target polynucleotides, particularly polynucleotides which alter cell phenotypes of induce or inhibit cell death. The method can be used to isolate toxic genes such as tumour suppressors. The present sequence was used to illustrate the method of the the present invention.
XX	
SQ	Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;
	Query Match            91.0%; Score 132; DB 22; Length 148; Best Local Similarity   98.0%; Pred. No. 6,6e-36; Matches 145; Conservative 0; Mismatches 0; Indels 3; Gaps 1.
QY	1 GGCCAAAATGTAACAGATCATTTATTGGACGGCGGCC--GTGATCCCCG 57
DB	1 GCCCAAAATTTAATAAACAGATCATTTATTGGACGGCGCCCATGCTGCATCCCCG 60
QY	58 GGCTCAGGAATTCGATATCAAGCTTATCGATACGTCGACCCTCGAGGGGGCCTTA 117       61 GGCTCAGGAATTCGATATCAAGCTTATCGATACGTCGACCCTCGAGGGGGCCTTA 120
QY	118 AACTAATTTTGTGTTTTGTGGCGCGCC 145       121 AACTAATTTTGTGTTTTGTGGCGCGCC 148
DB	
	RESULT 6
AAD31779	
ID	AAD31779 standard; DNA; 148 BP.
XX	
AC	AAD31779;
XX	
DT	18-JUN-2002 (first entry)
XX	
DE	Modified p7.5/tk vector, p7.5/ATG1/tk.
XX	
KM	Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
KW	vaccine; immune response; cytosstatic; p7.5/tk vector; thymidine kinase;
RN	p7.5/ATG1/tk vector; ds.
XX	
OS	Vaccinia virus.
OS	Synthetic.
PH	Key Location/Qualifiers

Query	Match	Best Local Similarity	Matches	145; Conservative	Score 132; DB 24; Length 148;	91.0%; Pred. No. 6,6e-36;	Indels 0;	Gaps 3;	1
0Y	1	GGCCAAAATTTGAAAACAGATCTATTTATTCAGCGGCGCC---	GTGATCCCCCG	57					
Db	1	GGCCAAAATTTGAAAACAGATCTATTTATTCAGCGGCGCCGCCATGATGATCCCGG	60						
0Y	58	GGCTGAGGAATTCGATATCAAGCTTATCGATACGCTCGACCTCGAGGGGGGACTACT	117						

Db 61 GCGTCAGGAATTCGATATACGCTTATCGATACCGTCGACCTGAGGGGGCCCTAACT 120  
 QY 118 AACTAATTTTGTGTTGGCGCCGCC 145  
 |||||||  
 Db 121 AACTAATTTTGTGTTGGCGCCGCC 148

RESULT 7  
 ID AAA15237  
 ID AAA15237 standard; DNA; 149 BP.

XX AAA15237;

AC 04-SEP-2000 (first entry)

DT Nucleotide sequence of a fragment of the plasmid p7.5/ATG2/tk.

XX Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;  
 KM vaccine; tumour regression; cancer; infection; ss.

XX Synthetic.

OS WO200028016-A1.

XX 18-MAY-2000.

XX 10-NOV-1998; 98WO-US24029.

XX 10-NOV-1998; 98WO-US24029.

XX (UYRP ) UNIV ROCHESTER.

XX Zauderer M;

XX WPI; 2000-376533/32.

PT Novel method of identifying target epitopes or antigens specific for  
 PT human tumors, cancers and infected cells involving screening expression  
 PT library products of a cell expressing the target epitope -  
 PS Disclosure; Fig 2; 132pp; English.

XX The present sequence represents a fragment of a vaccinia transfer  
 CC plasmid, which is used in the course of the invention. The  
 CC specification describes a method for identifying a target epitope.  
 CC The method comprises screening the products of an expression library  
 CC from a cell expressing the target epitope with cytotoxic T cells  
 CC generated against the cell to identify DNA clones expressing the target  
 CC epitope. The method may also comprise providing a cytotoxic T cell  
 CC specific for a gene product differentially expressed by a cell and  
 CC measuring the cross-reactivity of the cytotoxic T cell. The methods are  
 CC useful for identifying tumour specific target epitopes and antigens which  
 CC are useful in immunogenic compositions or vaccines to induce the  
 CC regression of tumors, cancers or infections in mammals. The genes  
 CC expressed in a panel of tumour cells that are derived from single  
 CC immortalised, non-tumorigenic cell line are used to generate HLA  
 CC restricted cytotoxic T cells which are evaluated for activity against  
 CC tumour cells. The method is useful to identify potential antigens  
 CC expressed not only by the pathogen but also by the host cells whose gene  
 CC expression is altered as a result of infection. The differential gene  
 CC expression strategies can be applied to identify immunogenic molecules  
 CC of cells infected with virus, fungus or mycobacterium.

XX Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;

Query Match 90.3%; Score 131; DB 21; Length 149;

Best Local Similarity 97.3%; Pred. No. 1.5e-35;

Matches 145; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
 QY 1 GGCACAAAATTTGAAAACACTGATCTATTATTTGACGCGCGCCGCC---CTGATCCCCC 56  
 |||||||  
 Db 1 GGCACAAAATTTGAAAACACTGATCTATTATTTGACGCGCGCGCCGCAAGTGCATCCCCC 60

QY 57 GGGCTGACGGAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGCCCTAAC 116  
 |||||||  
 Db 61 GGGCTGACGGAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGCCCTAAC 120  
 QY 117 TAACTAATTTTGTGTTGGCGCCGCC 145  
 |||||||  
 Db 121 TAACTAATTTTGTGTTGGCGCCGCC 149

RESULT 8  
 ID ABA01478  
 ID ABA01478 standard; DNA; 149 BP.

XX ABA01478;

AC 04-FEB-2002 (first entry)

DT Partial p7.5/ATG2/tk sequence.

XX Cell death; toxic gene; tumour suppressor; ds.

XX Synthetic.

XX WO200172995-A2.

XX 04-OCT-2001.

XX 28-MAR-2001; 2001WO-US09953.

XX 28-MAR-2000; 2000US-0192586.

XX 10-MAY-2000; 2000US-0203343.

XX 23-JAN-2001; 2001US-0263226.

XX 27-FEB-2001; 2001US-0271426.

XX (UYRP ) UNIV ROCHESTER.

XX Zauderer M, Smith BS;

XX WPI; 2001-570897/64.

PT Selecting target polynucleotides, particularly toxic genes, involves  
 PT introducing a library of insert polynucleotides into a host cell -  
 PT population, where the target polynucleotide promotes cell death -  
 PS Disclosure; Fig 8; 359pp; English.

XX The present invention relates to a method for selecting a target  
 CC polynucleotide. The method comprises introducing into a host cell  
 CC population a library of insert polynucleotides, where expression of the  
 CC target polynucleotide directly or indirectly promotes host cell death.  
 CC The cells are cultured and the insert polynucleotides are collected from  
 CC the cells which die. The method is useful for selecting target  
 CC polynucleotides, particularly polynucleotides which alter cell phenotypes  
 CC of induce or inhibit cell death. The method can be used to isolate toxic  
 CC genes such as tumour suppressors. The present sequence was used to  
 CC illustrate the method of the present invention.

XX Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;

Query Match 90.3%; Score 131; DB 22; Length 149;

Best Local Similarity 97.3%; Pred. No. 1.5e-35;

Matches 145; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 GGCACAAAATTTGAAAACACTGATCTATTATTTGACGCGCGCCGCC---GTGATCCCCC 56  
 |||||||  
 Db 1 GGCACAAAATTTGAAAACACTGATCTATTATTTGACGCGCGCGCCGCAAGTGCATCCCCC 60  
 QY 57 GGGCTGACGGAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGCCCTAAC 116  
 |||||||  
 Db 61 GGGCTGACGGAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGCCCTAAC 120  
 QY 117 TAACTAATTTTGTGTTGGCGCCGCC 145  
 |||||||

Db 121 TAACTAATTTGTTGTGGGCCGCC 149

RESULT 9

AAAD31780

ID AAD31780 standard; DNA: 149 BP.

XX

AC AAD31780;

XX

DT 18-JUN-2002 (first entry)

XX

DE Modified p7.5/tk vector, p7.5/ATG2/tk.

XX

KW Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;

KM vaccine; immune response; cytostatic; p7.5/tk vector; thymidine kinase;

KM p7.5/ATG2/tk vector; ds.

XX

OS Vaccinia virus.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT misc\_signal 46..48

FT /tag= a

FT /note= "translation start codon"

FT 117..119

FT /tag= b

FT /note= "translation stop codon"

FT 121..123

FT /tag= c

FT /note= "translation stop codon"

FT 125..127

FT /tag= d

FT /note= "translation stop codon"

FT 133..139

FT /tag= e

FT /note= "transcription stop signal"

XX

PN US2002018785-A1.

XX

PD 14-FEB-2002.

XX

PF 02-APR-2001; 2001US-0822250.

XX

PR 22-SEP-1997; 97US-0935377.

XX

PA (UYRP ) UNIV ROCHESTER.

XX

PI Zauderer M;

XX

DR WPI; 2002-239252/29.

XX

PT Representational Difference Analysis method for identification of

PT antigens recognized by cytotoxic T cells and specific for human tumors,

PT comprises improved selection of genes encoding target antigens -

XX

PS Example 1; Fig 2; 54pp; English.

XX

CC The present invention relates to novel methods for the identification

CC of antigens recognised by cytotoxic T cells (CTLs) and specific for

CC human tumours, cancers and infected cells. The method involves screening

CC the products of an expression library generated from DNA/RNA of a cell

CC expressing a target epitope with cytotoxic T cells generated against

CC the cell to identify DNA clones expressing target epitope or providing

CC cytotoxic T cells specific for a gene product differentially expressed

CC by a cell and measuring the cross-reactivity of the cytotoxic T cells

CC for cells expressing a target epitope in which the target epitope is

CC identified as a gene product inducing cytotoxic T cells. The method is

CC useful for identifying a target epitope or antigen specific for a tumour

CC cell. The target epitope is also useful for identifying target antigens

CC in other target cells against which it is desirable to induce cell-

CC mediated immunity. The antigen identified by the method is useful

CC in immunogenic compositions and vaccine preparations to induce the

CC regression of tumours, cancers and infections in mammals. The invention

CC also relates to vaccinia viral vectors which are useful for treating

CC tumour-bearing mammals, including humans to generate immune response

CC against the tumour cells. They are also useful for immunising or

CC vaccinating tumour-free subjects to prevent tumour formation. The

CC present sequence is modified p7.5/tk (thymidine kinase) vector,

CC p7.5/ATG2/tk. This vector comprises a vaccinia virus 7.5K promoter and

CC a modified tk DNA fragment. This vector is used in the exemplification

CC of the invention.

XX

SQ Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;

XX

Query Match 90.3%; Score 131; DB 24; Length 149;

Best Local Similarity 97.3%; Pred. No. 1.5e-35;

Matches 145; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

XX

QY 1 GGGCAAAATTTGAAAACAGATCTATTATGACGCGCGGCC---GTGGATCCCC 56

Db 1 GGGCAAAATTTGAAAACAGATCTATTATGACGCGCGGCCCATGATGATCCCC 60

QY 57 GGGCTGCAGGAATGCAATGCAAGCTTATGATACCGTCGACCTCGAGGGGGGCTTAAC 116

Db 61 GGGCTGCAGGAATGCAATGCAAGCTTATGATACCGTCGACCTCGAGGGGGGCTTAAC 120

QY 117 TAACTAATTTGTTGTGGGCCGCC 145

Db 121 TAACTAATTTGTTGTGGGCCGCC 149

XX

RESULT 10

AAAI5238

ID AAI5238 standard; DNA: 150 BP.

XX

AC AAI5238;

XX

DT 04-SEP-2000 (first entry)

XX

DE Nucleotide sequence of a fragment of the plasmid p7.5/ATG3/tk.

XX

KW Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;

KW vaccine; tumour regression; cancer; infection; ss.

XX

OS Synthetic.

XX

PN WO200028016-A1.

XX

PD 18-MAY-2000.

XX

PF 10-NOV-1998; 98WO-US24029.

XX

PR 10-NOV-1998; 98WO-US24029.

XX

PA (UYRP ) UNIV ROCHESTER.

XX

PI Zauderer M;

XX

DR WPI; 2000-376533/32.

XX

PT Novel method of identifying target epitopes or antigens specific for

PT human tumors, cancers and infected cells involving screening expression

PT library products of a cell expressing the target epitope -

XX

PS Disclosure; Fig 2; 132pp; English.

XX

CC The present sequence represents a fragment of a vaccinia transfer

CC plasmid, which is used in the course of the invention. The

CC specification describes a method for identifying a target epitope.

CC The method comprises screening the products of an expression library

CC from a cell expressing the target epitope with cytotoxic T cells

CC generated against the cell to identify DNA clones expressing the target

CC epitope. The method may also comprise providing a cytotoxic T cell

CC specific for a gene product differentially expressed by a cell and

CC measuring the cross-reactivity of the cytotoxic T cell. The methods are

CC useful for identifying tumour specific target epitopes and antigens which



PT antigens recognized by cytotoxic T cells and specific for human tumors,  
PT comprises improved selection of genes encoding target antigens -  
XX  
XX  
PS Example 1; Fig 2; 54pp; English.

XX The present invention relates to novel methods for the identification  
CC of antigens recognised by cytotoxic T cells (CTLs) and specific for  
CC human tumours, cancers and infected cells. The method involves screening  
CC the products of an expression library generated from DNA/RNA of a cell  
CC expressing a target epitope with cytotoxic T cells generated against  
CC the cell to identify DNA clones expressing target epitope or providing  
CC cytotoxic T cells specific for a gene product differentially expressed  
CC by a cell and measuring the cross-reactivity of the cytotoxic T cells  
CC for cells expressing a target epitope in which the target epitope is  
CC identified as a gene product inducing cytotoxic T cells. The method is  
CC useful for identifying a target epitope or antigen specific for a tumour  
CC cell. The target epitope is also useful for identifying target antigens  
CC in other target cells against which it is desirable to induce cell-  
CC mediated immunity. The antigen identified by the method is useful  
CC in immunogenic compositions and vaccine preparations to induce the  
CC regression of tumours, cancers and infections in mammals. The invention  
CC also relates to vaccinia viral vectors which are useful for treating  
CC tumour-bearing mammals, including humans to generate immune response  
CC against the tumour cells. They are also useful for immunising or  
CC vaccinating tumour-free subjects to prevent tumour formation. The  
CC present sequence is modified p7.5/tk (thymidine kinase) vector.  
CC p7.5/TK3/tk. This vector comprises a vaccinia virus 7.5K promoter and  
CC a modified tk DNA fragment. This vector is used in the exemplification  
CC of the invention.

XX Sequence 150 BP; 36 A; 38 C; 39 G; 37 T; 0 other;

XX  
XX Query Match 89.7%; Score 130; DB 24; Length 150;  
Best Local Similarity 96.7%; Pred. No. 3.3e-35;  
Matches 145; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 GGCACAAATTTGAAACCTAGATCTATTATTGACGCGGCCGCGC-----CGTGATCCCC 55  
DB 1 GGCACAAATTTGAAACCTAGATCTATTATTGACGCGGCCGCGCATGATGATCCCC 60  
QY 56 GGGGCTGAGGAATTCGATCAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAA 115  
DB 61 GGGGCTGAGGAATTCGATCAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAA 120  
QY 116 CTAACATAATTTGTTTGTGTTGGCGCCGCC 145  
DB 121 CTAACATAATTTGTTTGTGTTGGCGCCGCC 150

RESULT 13  
ABV33323  
ID ABV33323 standard; cDNA; 460 BP.  
XX  
AC ABV33323;  
XX  
DT 16-SEP-2002 (first entry)  
XX  
DE Human prostate expression marker cDNA 33314.  
XX  
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
XX pharmacogenomic marker; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200160860-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-US05171.  
XX  
PR 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAY-2000; 2000US-207454P.  
PR 18-JUL-2000; 2000US-211314P.

PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Schlegel R, Endege WO, Monahan JE;

XX WPI; 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer -  
XX  
XX

PS Claim 1; Page 7060-7061; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

SQ Sequence 460 BP; 118 A; 119 C; 114 G; 109 T; 0 other;

XX  
XX Query Match 49.4%; Score 71.6; DB 23; Length 460;  
Best Local Similarity 89.5%; Pred. No. 7.7e-15;  
Matches 77; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 46 GTGATCCCCCGGGCGTGCAGGAATTCGATCAGCTTATCGATACCGTGCAGAG 105  
DB 355 GTGATCCCCCGGGCGTGCAGGAATTCGATCAGCTTATCGATACCGTGCAGAG 414

QY 106 GGGGGCCTAAGTAATTTGTTT 131  
DB 415 GGGGGCCCGGTACCCAGCTTGTGTT 440

RESULT 14  
ABV42246  
ID ABV42246 standard; cDNA; 460 BP.  
XX  
AC ABV42246;  
XX  
DT 16-SEP-2002 (first entry)  
XX  
DE Human prostate expression marker cDNA 42237.  
XX  
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
XX pharmacogenomic marker; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200160860-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-US05171.  
XX  
PR 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAY-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.

PR 13-DEC-2000; 2000US-255281P.  
XX  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
PI Schlegel R, Endege WO, Monahan JE;  
XX  
DR WPI: 2001-662795/76.  
XX  
PT Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer  
XX  
PS Claim 1; Page 8465; 11750pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
XX  
SQ Sequence 460 BP; 118 A; 119 C; 114 G; 109 T; 0 other;  
XX  
Query Match 49.4%; Score 71.6; DB 23; Length 460;  
Best Local Similarity 89.5%; Pred. No. 7.7e-15;  
Matches 77; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
XX  
QY 46 GTGATCCCCCGGCTGCAGAAATTCGATCACTATGATACCTGACCTGAGG 105  
DB 355 GTGATCCCCCGGCTGCAGAAATTCGATCACTATGATACCTGACCTGAGG 414  
QY 106 GGGGGCTAAGTAAGTAATTTGTTT 131  
DB 415 GGGGGCCCGGTACCCAGCTTTGTTT 440  
XX  
RESULT 15  
ABV39281  
ID ABV39281 standard; CDNA: 508 BP.  
XX  
AC ABV39281;  
XX  
DT 16-SEP-2002 (first entry)  
XX  
DE Human prostate expression marker CDNA 39272.  
XX  
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200160860-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-US05171.  
XX  
PR 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAY-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.  
XX

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
PI Schlegel R, Endege WO, Monahan JE;  
XX  
DR WPI: 2001-662795/76.  
XX  
PT Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer  
XX  
PS Claim 1; Page 7972; 11750pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
XX  
SQ Sequence 508 BP; 140 A; 115 C; 125 G; 128 T; 0 other;  
XX  
Query Match 48.8%; Score 70.8; DB 23; Length 508;  
Best Local Similarity 82.7%; Pred. No. 1.5e-14;  
Matches 81; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
XX  
QY 33 GCACGGGGGCGCGTGCAGATCCCCGGGCTGCAGAAATTCGATCACTATGATAC 92  
DB 207 GCGGCCGCTGGAAGTGCATCCCCGGGCTGCAGAAATTCGATCACTATGATAC 266  
QY 93 GTGACCTCGAGGGGGGCTAAGTAATTTGTTT 130  
DB 267 GTGACCTCGAGGGGGGCGGTACCCAGCTTTGTTT 304  
XX

Search completed: November 10, 2002, 05:58:27  
Job time : 173.087 secs







```
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
; TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
; FILE REFERENCE: 1821.0070004
; CURRENT APPLICATION NUMBER: US/09/987,456
; PRIOR APPLICATION NUMBER: 2001-11-14
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/262,067
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/298,087
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/249,268
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 145
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p 7.5/ATG0/tk promoter
US-09-987-456-2

Query Match
Best Local Similarity 100.0%; Score 145; DB 10; Length 145;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 1 GGCCTAAATTTGAAACCTAGATCTATTATTGACAGCGCGCGCGTGATCCCCGGGC 60
    |||||||
Db 1 GGCCTAAATTTGAAACCTAGATCTATTATTGACAGCGCGCGCGTGATCCCCGGGC 60

Oy 61 TGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGGGGCTACTAAC 120
    |||||||
Db 61 TGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGGGGCTACTAAC 120

Oy 121 TAATTTGTTTTTGTGGGCCGGCC 145
    |||||||
Db 121 TAATTTGTTTTTGTGGGCCGGCC 145
```

```
RESULT 3
US-09-822-250-7
; Sequence 7, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 148
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-822-250-7
```

```
Query Match
Best Local Similarity 91.0%; Score 132; DB 10; Length 148;
Matches 145; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Oy 1 GGCCTAAATTTGAAACCTAGATCTATTATTGACAGCGCGCGCGTGATCCCCGG 57
    |||||||
Db 1 GGCCTAAATTTGAAACCTAGATCTATTATTGACAGCGCGCGCGTGATCCCCGG 60

Oy 58 GGCCTAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGGGGCTAACT 117
    |||||||
```

```
Db 61 GGCCTAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGGGGCTAACT 120
Oy 118 AACTAATTTGTTTTGTGGGCCGGCC 145
    |||||||
Db 121 AACTAATTTGTTTTGTGGGCCGGCC 148
```

```
RESULT 4
US-09-987-456-3
; Sequence 3, Application US/09987456
; Patent No. US20020123057A1
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
; TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
; FILE REFERENCE: 1821.0070004
; CURRENT APPLICATION NUMBER: US/09/987,456
; PRIOR APPLICATION NUMBER: 2001-11-14
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/271,424
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/298,087
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/249,268
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 148
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p 7.5/ATG1/tk promoter
US-09-987-456-3
```

```
Query Match
Best Local Similarity 91.0%; Score 132; DB 10; Length 148;
Matches 145; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Oy 1 GGCCTAAATTTGAAACCTAGATCTATTATTGACAGCGCGCGCGTGATCCCCGG 57
    |||||||
Db 1 GGCCTAAATTTGAAACCTAGATCTATTATTGACAGCGCGCGCGTGATCCCCGG 60

Oy 58 GGCCTAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGGGGCTAACT 117
    |||||||
Db 61 GGCCTAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGGGGCTAACT 120

Oy 118 AACTAATTTGTTTTGTGGGCCGGCC 145
    |||||||
Db 121 AACTAATTTGTTTTGTGGGCCGGCC 148
```

```
RESULT 5
US-09-822-250-8
; Sequence 8, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 149
; TYPE: DNA
; ORGANISM: synthetic construct
```

US-09-822-250-8

Query Match	90.3%;	Score 131;	DB 10;	Length 149;
Best Local Similarity	97.3%;	Pred. No. 4.8e-40;		
Matches 145;	Conservative 0;	Mismatches 0;	Indels 4;	Gaps 1;

Qy	1	GGCCAAAATTGAAAACCTGATCATTTATTTTGTGACGGCGGCCGCGC	---	-GTGGATCCCC	56
Db	1	GGCCAAAATTGAAAACCTGATCATTTATTTTGTGACGGCGGCCGCGCATGATGATCCCC			60
Qy	57	GGCGTCGACGAGAAATTCGATATCACTTATCGATTCGCTGCACCTCGAGGGGGGGCCTAAC			116
Db	61	GGCGTCGACGAGAAATTCGATATCACTTATCGATTCGCTGCACCTCGAGGGGGGGCCTAAC			120
Qy	117	TAACATAATTTTGTTTTGTGTGGCGCCGGGCC			145
Db	121	TAACATAATTTTGTTTTGTGTGGCGCCGGGCC			149

RESULT 6  
US-09-987-456-4

	Matches	145: Conservative	0: Mismatches	0: Indels	4: Gaps
QY	1	GGCCAAAATGAAAAATCAGTATCTATTATTGTCAGCGGGCGGGC-----GTGATCCCC	56		
Db	1	GGCCAAAATGAAAAATCAGTATCTATTATTGTCAGCGGGCGGGCAGATGATCCCC	60		
QY	57	GGGCTGCAGGAATTCGATTCACGCTTATCGATACGCTCGAGGGGGGGCCCTAAC	116		
Db	61	GGGCTGCAGGAATTCGATTCACGCTTATCGATACCGTCGAGGGGGGGGGCCCTAAC	120		

RESULT 7  
US-09-822-250-9  
; Sequence 9, Application US/09822250  
; Patent No. US70020018785A1  
; GENERAL INFORMATION:  
; APPLICANT: Zauderer, Maurice

```

: TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
: FILE REFERENCE: 1821.0010001
: CURRENT APPLICATION NUMBER: US/09/822,250
: CURRENT FILING DATE: 2001-04-02
: PRIOR APPLICATION NUMBER: US 08/935,377
: PRIOR FILING DATE: 1997-09-22
: NUMBER OF SEQ. ID NOS: 37
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 9
: LENGTH: 150
: TYPE: DNA
: ORGANISM: synthetic construct
: US-09-822-250-9

Query Match      89.7%; Score 130; DB 10; Length 150;
Best Local Similarity 96.7%; Pred. No. 1,1e-39;
Matches 145; Conservative 0; Mismatches -3; Indels 5; Gaps 1;

```

Qy	1	GGCAAAATTTGAAAACTACATCTATTTATTTATGGACGGCCGC	----	-GTTGATATCC	55
Db	1	GCCCAAAATTTGAAAACTACATCTATTTATTTATGGACGGCCGC	ATGACACTG	ATATCC	60
Qy	56	CGGCTGACGAGATTCGATTCACAGCTTATGATACCGTGACCTCGAGGGGGGCTAA			115
Db	61	CGGCTGACGAGATTCGATTCACAGCTTATGATACCGTGACCTCGAGGGGGGCTAA			120
Qy	121	CTAACTAATTTTGTTTTGTGGGGCCG			145
Db	121	CTAACTAATTTTGTTTTGTGGGGCCG			150

RESULT 8  
 US-09-987-456-5  
 Sequence 5, Application US/09987456  
 Patent No. US20020123057A1  
 GENERAL INFORMATION:  
 APPLICANT: University of Rochester  
 APPLICANT: Zauderer, Maurice  
 APPLICANT: Ernest S. Smith  
 TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting  
 TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells  
 FILE REFERENCE: 1821.0070004  
 CURRENT APPLICATION NUMBER: US/09/987,456  
 CURRENT FILING DATE: 2001-11-14  
 PRIOR APPLICATION NUMBER: 60/271,424  
 PRIOR FILING DATE: 2001-02-27  
 PRIOR APPLICATION NUMBER: 60/262,067  
 PRIOR FILING DATE: 2001-01-18  
 PRIOR APPLICATION NUMBER: 60/298,087  
 PRIOR FILING DATE: 2001-06-15  
 PRIOR APPLICATION NUMBER: 60/249,268  
 PRIOR FILING DATE: 2000-11-17  
 NUMBER OF SEQ ID NOS: 147  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO 5  
 LENGTH: 150  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: p7.5/ATG3/ck vector  
 US-09-987-456-5

Query Match	89.78;	Score 130;	DB 10;	Length 150;
Best Local Similarity	96.78;	Pred. No. 1.1e-39;		
Matches 145; Conservative	0;	Mismatches	0;	Indels 5; Gaps 1.

0Y	1	GGCAAAATTGAAACCTGATCTATTTTATGACGGGGCCG	----	-GTTGGATCCC	55
Db	1	GGCAAAATTGAAACCTGATCTATTTTATGACGGGGCCG	CGCATGACGTGGATCCCC		60
0Y	56	CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGCACCTCGACGGGGGGGCCCTAA			115
1b	61	CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGCACCTCGACGGGGGGGCCCTAA			120

Oy 116 CTAACATAATTTGTTTGTGGCCCGGCC 145  
| | | | | | | | | | | | | | | | | | | |  
Db 121 CTAACATAATTTGTTTGTGGCCCGGCC 150

RESULT 9  
US-09-834-975-601/c

; Sequence 601, Application US/09834975  
; Patent No. US20020110815A1  
; GENERAL INFORMATION:  
; APPLICANT: Lillie, James  
; APPLICANT: Brown, Jeffrey  
; APPLICANT: Bolt, Andrew  
; APPLICANT: Van Huffel, Christophe  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS  
; TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY  
; TITLE OF INVENTION: OF HUMAN CANCERS  
; FILE REFERENCE: MRI-016B  
; CURRENT APPLICATION NUMBER: US/09/834,975  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 60/197,538  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 1046  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 601  
; LENGTH: 424  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-834-975-601

Query Match 47.6%; Score 69; DB 10; Length 424;  
Best Local Similarity 88.2%; Pred. No. 1.7e-16;  
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 46 GTGATCCCGGGCTGCAGATTCGATCAAGCTTATGATACCGTGCACCTCGAGC 105  
| | | | | | | | | | | | | | | | | | | |  
Db 104 GTGATCCCGGGCTGCAGATTCGATCAAGCTTATGATACCGTGCACCTCGAGC 45  
| | | | | | | | | | | | | | | | | | | |  
Oy 106 GGGGCGCTAATCACTAATTTGTT 130  
| | | | | | | | | | | | | | | | | | | |  
Db 44 GGGGCGCGGTACCCAGCTTTGTT 20

RESULT 10  
US-09-735-705-91

; Sequence 91, Application US/09735705  
; Patent No. US20020052329A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C14  
; CURRENT APPLICATION NUMBER: US/09/735,705  
; CURRENT FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 91  
; LENGTH: 858  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE: \*

; NAME/KEY: misc\_feature  
; LOCATION: (1)...(858)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-735-705-91

Query Match 47.3%; Score 68.6; DB 10; Length 858;  
Best Local Similarity 84.6%; Pred. No. 3.4e-16;  
Matches 77; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Oy 22 ATCTATTATTGACGCGCGCGGTGATCCCGGGCTGCAGGATTCGATATCAAGC 81  
| | | | | | | | | | | | | | | | | | | |  
Db 333 AACGAATCCACCCACACTGACTAGTGATCCCGGGCTGCAGGATTCGATATCAAGC 392  
| | | | | | | | | | | | | | | | | | | |  
Oy 82 TTATCGATACCGTCGACCTCGAGGGGGGCC 112  
| | | | | | | | | | | | | | | | | | | |  
Db 393 TTATCGATACCGTCGACCTCGAGGGGGGCC 423

RESULT 11  
US-09-850-716A-91

; Sequence 91, Application US/09850716A  
; Patent No. US2002015139A1  
; GENERAL INFORMATION:  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Retter, Marc W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C15  
; CURRENT APPLICATION NUMBER: US/09/850,716A  
; CURRENT FILING DATE: 2001-05-07  
; NUMBER OF SEQ ID NOS: 440  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 91  
; LENGTH: 858  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(858)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-850-716A-91

Query Match 47.3%; Score 68.6; DB 10; Length 858;  
Best Local Similarity 84.6%; Pred. No. 3.4e-16;  
Matches 77; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Oy 22 ATCTATTATTGACGCGCGCGGTGATCCCGGGCTGCAGGATTCGATATCAAGC 81  
| | | | | | | | | | | | | | | | | | | |  
Db 333 AACGAATCCACCCACACTGACTAGTGATCCCGGGCTGCAGGATTCGATATCAAGC 392  
| | | | | | | | | | | | | | | | | | | |  
Oy 82 TTATCGATACCGTCGACCTCGAGGGGGGCC 112  
| | | | | | | | | | | | | | | | | | | |  
Db 393 TTATCGATACCGTCGACCTCGAGGGGGGCC 423

RESULT 12  
US-09-897-778-91

; Sequence 91, Application US/09897778  
; Patent No. US20020147143A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Marnetakis, Margarita  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Peckham, David W.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C16

```

: CURRENT APPLICATION NUMBER: US/09/897,778
: CURRENT FILING DATE: 2001-06-28
: NUMBER OF SEQ ID NOS: 467
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 91
: LENGTH: 858
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 570, 591, 655, 664, 667, 683, 711, 759, 760, 765, 777, 787,
: LOCATION: 792, 794, 801, 804, 809, 817, 820
: OTHER INFORMATION: n = A,T,C or G
US-09-897-778-91

Query Match
Best Local Similarity 47.3%; Score 68.6; DB 10; Length 858;
Matches 77; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 22 ATCTATTATGTCACGGCGCGGTGATGTCCTCCCGGGCTGCAGGAATTCATATCAAGC 81
Db 333 AACGATTCCACACACACGACTGACTGTGATCCCCGGGCTGCAGGAATTCATATCAAGC 392
OY 82 TTATGATACCGTCGACCTCGAGGGGGGCC 112
Db 393 TTATGATACCGTCGACCTCGAGGGGGGCC 423

RESULT 13
US-09-784-130-9/C
: Sequence 9, Application US/09784130
: Patent No. US20020076808A1
: GENERAL INFORMATION:
: APPLICANT: Donahue, Brian A.
: APPLICANT: Hardy, Stephen F.
: APPLICANT: Snyder, Richard O.
: APPLICANT: Cell Genesys, Inc.
: TITLE OF INVENTION: USE OF SUPPRESSOR tRNA'S TO REGULATE CYTOTOXICITY
: FILE REFERENCE: F132222
: CURRENT APPLICATION NUMBER: US/09/784,130
: CURRENT FILING DATE: 2001-02-16
: PRIOR APPLICATION NUMBER: 60/097,328
: PRIOR FILING DATE: 1998-08-20
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 9
: LENGTH: 118
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: polylinker
US-09-784-130-9

Query Match
Best Local Similarity 46.2%; Score 67; DB 10; Length 118;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 46 GTGATCCCCCGGGCTGCAGGAATTCATATCAAGCTTATGATACCGTCGACCTCGAG 105
Db 91 GTGATCCCCCGGGCTGCAGGAATTCATATCAAGCTTATGATACCGTCGACCTCGAG 32
OY 106 GGGGGCC 112
Db 31 GGGGGCC 25

RESULT 14
US-09-735-705-306
: Sequence 306, Application US/09735705
: Patent No. US20020052329A1
: GENERAL INFORMATION:
```

```

: APPLICANT: Wang, Tongtong
: APPLICANT: Fan, Liqun
: APPLICANT: Kalos, Michael D.
: APPLICANT: Bangur, Chaitanya S.
: APPLICANT: Hosken, Nancy
: APPLICANT: Fanger, Gary R.
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Henderson, Robert A.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Fanger, Neil
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C14
: CURRENT APPLICATION NUMBER: US/09/735,705
: CURRENT FILING DATE: 2000-12-12
: NUMBER OF SEQ ID NOS: 419
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 306
: LENGTH: 457
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-735-705-306

Query Match
Best Local Similarity 46.2%; Score 67; DB 10; Length 457;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

OY 46 GTGATCCCCCGGGCTGCAGGAATTCATATCAAGCTTATGATACCGTCGACCTCGAG 105
Db 360 GTGATCCCCCGGGCTGCAGGAATTCATATCAAGCTTATGATACCGTCGACCTCGAG 419
OY 106 GGGGGCC 112
Db 420 GGGGGCC 426

RESULT 15
US-09-850-716A-306
: Sequence 306, Application US/09850716A
: Patent No. US20020115139A1
: GENERAL INFORMATION:
: APPLICANT: Kalos, Michael D.
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Retter, Marc W.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: FILE REFERENCE: 210121.455C15
: CURRENT APPLICATION NUMBER: US/09/850,716A
: CURRENT FILING DATE: 2001-05-07
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 306
: LENGTH: 457
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-850-716A-306

Query Match
Best Local Similarity 46.2%; Score 67; DB 10; Length 457;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 46 GTGATCCCCCGGGCTGCAGGAATTCATATCAAGCTTATGATACCGTCGACCTCGAG 105
Db 360 GTGATCCCCCGGGCTGCAGGAATTCATATCAAGCTTATGATACCGTCGACCTCGAG 419
OY 106 GGGGGCC 112
Db 420 GGGGGCC 426

Search completed: November 10, 2002, 11:33:45
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Job time : 38.087 secs

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```

LOCATION (765)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (777)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (787)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (792)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (794)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (801)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (804)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (809)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (817)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (820)
OTHER INFORMATION: where n is a, c, g or t
US-09-123-912-91

Query Match      47.3%, Score 68.6, DB 4; Length 858;
Best Local Similarity 84.6%; Pred. No. 3.le-14;
Matches 77; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY    22  ATCTTTATTATGACGGCGCCGCCGTGGATCCCCCGGCTGCAGGAATTTCATCAAGC 81
       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB    333  AACGAATTCACACACACTTGACTAATGATATCCCCC GGCGCTGCAGGAATTTCATCAAGC 392
       ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

OY    82  TTATCATACCGTCCGACCTCGAGGGGGGCC 112
       ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB    393  TTATCATACCTCGACCTCGAGGGGGGCC 423
       ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 4
US-09-643-597-91
Sequence 91, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
TITLE OF INVENTION: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455c11
CURRENT APPLICATION NUMBER: US/09/643.597
NUMBER OF SEQ ID NOS: 2000-08-21
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 91
LENGTH: 858
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
```





```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs.
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-124-698-121

Query Match
Best Local Similarity 47.0%; Score 68.2; DB 3; Length 793;
Matches 76; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 42 CGCCGTGATCCCCGGGCGTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTC 101
DB 122 CGGGCGGATCCCCGGGCGTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTC 63
QY 102 GAGGGGGGCGCTAATACTATTGTT 130
DB 62 GAGGGGGGCGCGGTACCAAGCTTTGTT 34
```

```
RESULT 8
US-09-127-480-121/c
Sequence 121, Application US/09127480
Patent No. 6194153
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
```

```
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-127-480-121
```

```
Query Match
Best Local Similarity 47.0%; Score 68.2; DB 4; Length 793;
Matches 76; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 42 CGCCGTGATCCCCGGGCGTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTC 101
DB 122 CGGGCGGATCCCCGGGCGTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTC 63
QY 102 GAGGGGGGCGCTAATACTATTGTT 130
DB 62 GAGGGGGGCGCGGTACCAAGCTTTGTT 34
```

```
RESULT 9
US-08-496-841C-121/c
Sequence 121, Application US/08496841C
Patent No. 6210919
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
```

```
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 175
```

```
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841C
FILING DATE: 28-Jun-1995
CLASSIFICATION: <Unknown>
```

```
ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehner, Ph.D.
REGISTRATION NUMBER: 35,135
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 753-6237
```

```
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 121:
US-08-496-841C-121
```

```
Query Match
Best Local Similarity 47.0%; Score 68.2; DB 4; Length 793;
Matches 76; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
```

```
QY 42 CGCCGTGATCCCCGGGCGTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTC 101
DB 122 CGGGCGGATCCCCGGGCGTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTC 63
```



APPLICANT: Dillon, Patrick J.  
APPLICANT: Choi, Gil H.  
APPLICANT: Welch, Rodney A.  
TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli  
Patent No. 6316609  
NUMBER OF SEQUENCES: 142  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Ave, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/976,259  
FILING DATE: Herewith  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/031,626 AND US 60/061,953  
ATTORNEY/AGENT INFORMATION:  
NAME: Steffe, Eric K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488, 0740002/EKS/CBM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 752 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-976-259-108

Query Match 46.2%; Score 67; DB 4; Length 752;  
Best Local Similarity 100.0%; Pred. No. 1e-13;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 GTGATCCCCCGGCTGCAGGATTCGATTCACCTTATCGATCCGTCGACCTCGAGG 105  
|||||  
DB 72 GTGATCCCCCGGCTGCAGGATTCGATTCACCTTATCGATCCGTCGACCTCGAGG 13  
QY 106 GGGGGCC 112  
|||||  
DB 12 GGGGGCC 6

RESULT 14  
US-08-446-935-6/C  
Sequence 6, Application US/08446935  
Patent No. 6187991  
GENERAL INFORMATION:  
APPLICANT: Soeller, Walter C.  
APPLICANT: Carly, Maynard D.  
APPLICANT: Kreuter, David K.  
TITLE OF INVENTION: TRANSGENIC ANIMAL MODELS FOR TYPE II  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pfizer Inc.  
STREET: 235 East 42nd Street, 20th Floor  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10017-5755  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,935  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Sheyka, Robert F.  
REGISTRATION NUMBER: 31,304  
REFERENCE/DOCKET NUMBER: PC8153  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)573-1189  
TELEFAX: (212)573-1939  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2961 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
US-08-446-935-6

Query Match 46.2%; Score 67; DB 4; Length 2961;  
Best Local Similarity 100.0%; Pred. No. 1.6e-13;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 GTGATCCCCCGGCTGCAGGATTCGATTCACCTTATCGATCCGTCGACCTCGAGG 105  
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DB 726 GTGATCCCCCGGCTGCAGGATTCGATTCACCTTATCGATCCGTCGACCTCGAGG 667  
QY 106 GGGGGCC 112  
|||||  
DB 666 GGGGGCC 660

RESULT 15  
US-08-992-334-1/C  
Sequence 1, Application US/08992334  
Patent No. 591678  
GENERAL INFORMATION:  
APPLICANT: Gruss, Alexandra  
APPLICANT: Maguin, Emmanuelle  
TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Christie Parker & Hale, LLP  
STREET: 350 West Colorado Boulevard, Suite 500  
CITY: Pasadena  
STATE: California  
COUNTRY: United States  
ZIP: 91105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/992,334  
FILING DATE: 17-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/302,752  
FILING DATE: 24-DEC-1994  
PRIOR APPLICATION DATA: PCT/FR93/00248  
APPLICATION NUMBER: PCT/FR93/00248  
FILING DATE: 12-MAR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 992/03034  
FILING DATE: 13-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Priout, D. Bruce

REGISTRATION NUMBER: 20958  
REFERENCE/DOCKET NUMBER: C93:31779  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (626) 795-9900  
TELEFAX: (626) 577-8800  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3792 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHEetical: NO  
ANTI-SENSE: YES  
IMMEDIATE SOURCE:  
CLONE: pc+host4  
US-08-992-334-1

Query Match 46.2%; Score 67; DB 2; Length 3792;  
Best Local Similarity 100.0%; Pred. No. 1,7e-13;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3541 GTGGATCCCCCGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTTCGACCTCGAGG 105  
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QY 106 GGGGGCC 112  
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Db 3481 GGGGGCC 3475

Search completed: November 10, 2002, 08:36:12  
Job time : 40.1739 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:05:45 ; Search time 719.586 Seconds

(without alignments)  
5985.683 Million cell updates/sec

Title: US-08-935-377-7

Sequence: 148  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_htg:\*  
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41: em\_htgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	148	100.0	148	6 AX326744	AX326744 Sequence
2	137	92.6	149	6 AX326745	AX326745 Sequence
3	136	91.9	150	6 AX326746	AX326746 Sequence
4	132	89.2	145	6 AX326743	AX326743 Sequence
5	70.6	47.7	858	6 AR176413	AR176413 Sequence
6	70.6	47.7	858	6 AX365698	AX365698 Sequence
7	69.8	47.2	259	6 AA4281	AA4281 Sequence 9
8	69.8	47.2	574	6 AX284736	AX284736 Sequence
9	69.4	46.9	424	6 AX284796	AX284796 Sequence
10	69.4	46.9	2059	12 AY034154	AY034154 Cloning v
11	69.4	46.9	2890	12 AB035274	AB035274 Homo sapi
12	69.4	46.9	2958	6 AX247548	AX247548 Sequence
13	69.4	46.9	2958	12 ARBLKSM	AX2326 Bluescript
14	69.4	46.9	2958	12 ARBLKSP	X52331 Bluescript
15	69.4	46.9	2961	12 ARBLKSM	X52329 Bluescript
16	69.4	46.9	2961	12 ARBLKSP	X52327 Bluescript
17	69.4	46.9	2964	12 SYNBKSMV	L08784 Bluescribe
18	69.4	46.9	2964	12 SYNBKSPV	L08785 Bluescribe
19	69.4	46.9	3306	12 SYNBKSPV	D85525 Cloning vec
20	69.4	46.9	3417	12 AF153422	AF153422 Cloning v
21	69.4	46.9	3485	12 AF178449	AF178449 Integrat
22	69.4	46.9	4144	12 XXU35131	U35131 Plasmid pbs
23	69.4	46.9	4267	12 PRS304	U03436 Yeast integ
24	69.4	46.9	4289	12 XXU35136	U03136 Plasmid pbs
25	69.4	46.9	4373	12 PRS306	U03438 Yeast integ
26	69.4	46.9	4443	12 PRS303	U03435 Yeast integ
27	69.4	46.9	4549	12 AF178452	AF178452 Integrat
28	69.4	46.9	4670	12 ASAU5326	AJ005326 pGAT1(+)
29	69.4	46.9	4670	12 ASAU5329	AJ005329 pGAT1(-)
30	69.4	46.9	4707	12 XXU02374	U02374 Cloning vec
31	69.4	46.9	4768	12 XXU25061	U25061 Cloning vec
32	69.4	46.9	4783	12 PRS316	U03440 Yeast cent
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34	69.4	46.9	4950	12 XXU25060	U25060 Cloning vec
35	69.4	46.9	4967	12 PRS313	U03439 Yeast cent
36	69.4	46.9	5144	12 CVU23751	U23751 Cloning vec
37	69.4	46.9	5187	12 U34687	U34687 Yeast integ
38	69.4	46.9	5228	12 XXU25059	U25059 Cloning vec
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40	69.4	46.9	5634	12 CVU14125	U14125 Cloning vec
41	69.4	46.9	5973	12 AF504908	AF504908 Cloning v
42	69.4	46.9	6018	12 PRS315	U03441 Yeast cent
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45	68.8	46.5	2961	12 CVU46017	U46017 Cloning vec

ALIGNMENTS

RESULT 1  
LOCUS AX326744 148 bp DNA  
DEFINITION Sequence 5 from Patent WO0172995.  
ACCESSION AX326744  
VERSION AX326744.1 GI:18097470  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct.  
artificial sequences.  
REFERENCE  
AUTHORS Zauderer, M. and Smith, E.S.  
TITLE Methods of producing a library and methods of selecting polynucleotides of interest  
JOURNAL Patent: WO 0172995-A 5 04-OCR-2001;

Pred. No. is the number of results predicted by chance to have a

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    location/Qualifiers
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    /db_xref="taxon:32630"
    /note="Nucleotide Sequence of p7.5/ATG1/LK"
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  Best Local Similarity 100.0%; Pred. No. 2.2e-35;
  Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCAAAATGAAAACATAGATCTATTATTGACGGCGCCGACATGATGATCCCCG 60
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Db 1 GGGCAAAATGAAAACATAGATCTATTATTGACGGCGCCGACATGATGATCCCCG 60

OY 61 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAACT 120
    |||||||
Db 61 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAACT 120

OY 121 AACTAATTTGTTTGTGGCCCGGCC 148
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Db 121 AACTAATTTGTTTGTGGCCCGGCC 148

RESULT 2
AX326745 149 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 6 from Patent WO0172995.
ACCESSION AX326745
VERSION AX326745.1 GI:18097471
KEYWORDS
  .
  synthetic construct.
  synthetic construct
  artificial sequences.
REFERENCE
  1
  Zauderer,M. and Smith,E.S.
  Methods of producing a library and methods of selecting
  polynucleotides of interest
  Patent: WO 0172995-A 6 04-OCT-2001;
  JOURNAL UNIVERSITY OF ROCHESTER (US)
  location/Qualifiers
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  /note="Nucleotide Sequence of p7.5/ATG2/LK"
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    92.6%; Score 137; DB 6; Length 149;
  Best Local Similarity 99.3%; Pred. No. 5.9e-32;
  Matches 148; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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    |||||||
Db 1 GGGCAAAATGAAAACATAGATCTATTATTGACGGCGCCGACATGATGATCCCC 60

OY 60 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAACT 119
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Db 61 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAACT 120

OY 120 TAACTAATTTGTTTGTGGCCCGGCC 148
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KEYWORDS
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  synthetic construct.
  synthetic construct
  artificial sequences.
REFERENCE
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  Zauderer,M. and Smith,E.S.
  Methods of producing a library and methods of selecting
  polynucleotides of interest
  Patent: WO 0172995-A 7 04-OCT-2001;
  JOURNAL UNIVERSITY OF ROCHESTER (US)
  location/Qualifiers
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  /note="Nucleotide Sequence of p7.5/ATG3/LK"
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  Best Local Similarity 98.7%; Pred. No. 1.2e-31;
  Matches 148; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

OY 1 GGGCAAAATGAAAACATAGATCTATTATTGACGGCGCCGACATGATGATCCCC 58
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OY 59 CGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAA 118
    |||||||
Db 61 CGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAA 120

OY 119 CTAATAATTTGTTTGTGGCCCGGCC 148
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Db 121 CTAATAATTTGTTTGTGGCCCGGCC 150

RESULT 4
AX326743 145 bp DNA linear PAT 07-JAN-2002
LOCUS AX326743
DEFINITION Sequence 4 from Patent WO0172995.
ACCESSION AX326743
VERSION AX326743.1 GI:18097469
KEYWORDS
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  synthetic construct.
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SOURCE
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  artificial sequences.
ORGANISM
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  artificial sequences.
REFERENCE
  1
  Zauderer,M. and Smith,E.S.
  Methods of producing a library and methods of selecting
  polynucleotides of interest
  Patent: WO 0172995-A 4 04-OCT-2001;
  JOURNAL UNIVERSITY OF ROCHESTER (US)
  location/Qualifiers
  1.145
  /organism="synthetic construct"
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  Best Local Similarity 98.0%; Pred. No. 2.1e-30;
  Matches 145; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

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Db 1 GGGCAAAATGAAAACATAGATCTATTATTGACGGCGCCGACATGATGATCCCC 57

OY 61 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAACT 120
    |||||||
Db 58 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAACT 117

OY 121 AACTAATTTGTTTGTGGCCCGGCC 148
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DB	118	AACTAATTTTCTTTTGTGGCCGCC	145
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LOCUS	ARI16413		Linear
DEFINITION	Sequence 91 from patent US 6312695.		PAT 17-DEC-2001
ACCESSION	ARI16413		
VERSION	ARI16413.1	GI:17918768	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 858)		
TITLE	Reed, S.G. and Wang, T.Tong.		
JOURNAL	Compounds and methods for therapy of lung cancer		
FEATURES	Patent: US 6312695-A 91 06-NOV-2001;		
source	location/Qualifiers		
	1..858		
BASE COUNT	196 a 212 c 193 g 238 t	19 others	
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Query Match	47.7%;	Score 70.6;	DB 6;
Best Local Similarity	84.9%;	Pred. No. 3.3e-11;	Length 858;
Matches	79; Conservative	0; Mismatches	14; Indels
			Gaps 0;
QY	23 TCTATTATTATTCGACGCGCCCATGTGATCCCGCGGCTGCAGAAATTCGATATCAA	82	
DB	331 TCACGAAATTCACACACACTGCAGCTAGTGTGATCCCGCGGCTGCAGAAATTCGATATCAA	390	
QY	83 GCTTATCGATACCGTCGACCTCGAGGGGGGCC	115	
DB	391 GCTTATCGATACCGTCGACCTCGAGGGGGGCC	423	
RESULT 6	AX365698	858 bp	DNA
LOCUS	AX365698		Linear
DEFINITION	Sequence 91 from Patent WO200174.		PAT 15-FEB-2002
ACCESSION	AX365698		
VERSION	AX365698.1	GI:18697250	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1		
JOURNAL	Wang, T., Wang, A., Skelky, Y.A., Li, S.X., Kalos, M.D., Henderson, R.A.,		
FEATURES	McNeill, P.D., Fanger, N., Retter, M.W., Marnettakis, M., Fanger, G.R.,		
source	Vevelick, T.S., Carter, D., Watanabe, Y. and Peckham, D.W.		
	Compositions and methods for the therapy and diagnosis of lung		
	cancer		
	Patent: WO 0200174-A 91 03-JAN-2002;		
	CORIXA CORPORATION (US)		
	location/Qualifiers		
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BASE COUNT	196 a 212 c 193 g 238 t	19 others	
ORIGIN	1		
Query Match	47.7%;	Score 70.6;	DB 6;
Best Local Similarity	84.9%;	Pred. No. 3.3e-11;	Length 858;
Matches	79; Conservative	0; Mismatches	14; Indels
			Gaps 0;
QY	23 TCTATTATTATTCGACGCGCCCATGTGATCCCGCGGCTGCAGAAATTCGATATCAA	82	
DB	331 TCACGAAATTCACACACACTGCAGCTAGTGTGATCCCGCGGCTGCAGAAATTCGATATCAA	390	
QY	83 GCTTATCGATACCGTCGACCTCGAGGGGGGCC	115	
DB	391 GCTTATCGATACCGTCGACCTCGAGGGGGGCC	423	

LOCUS	AA4281	259 bp	DNA	linear	PAT 07-MAR-1997
DEFINITION	Sequence 9 from Patent WO9511300.				
ACCESSION	A44281				
VERSION	A44281.1 GI:2299115				
KEYWORDS	.				
SOURCE	unidentified.				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 259)				
AUTHORS	Chandley,A.C., Kun,M., Sharkey,A.M., Hargreave,T.B. and Cooke,H.J.				
TITLE	AZOOSPERMIA IDENTIFICATION AND TREATMENT				
JOURNAL	Patent: WO 9511300-A 9 27-APR-1995;				
COMMENT	MEDICAL RES COUNCIL (GB) 794/794 950508.				
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Best Local Similarity	79.0% Pred. NO.4.8e-11;				
Matches	83; Conservative	0;	Mismatches	22;	Indels 0; Gaps 0;
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Db	132	TAAAGCAAGCAAGCGCTCTAGTGATCCCGCGGCGTCAGAAATTCGATATCAAGCTTAT	73		
OY	89	CGATCCGCTGCAGCTCGAGGGGGGCTAACTAATTTGTT	133		
Db	72	CGATACCTGCAGCTCGAGGGGGGCGCGTACCAGCTTTGTT	28		
RESULT 8					
LOCUS	AX284736	574 bp	DNA	linear	PAT 20-NOV-2001
DEFINITION	Sequence 541 from Patent WO0179556.				
ACCESSION	AX284736				
VERSION	AX284736.1 GI:17045424				
KEYWORDS	.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1				
AUTHORS	Lillie,J., Brown,J.L., Bolt,A. and van Hufel,C.				
TITLE	Novel genes, compositions and methods for the identification,				
JOURNAL	assessment, prevention, and therapy of human cancers				
	Patent: WO 0179556-A 541 25-OCT-2001;				
FEATURES	Millennium Predictive Medicine, Inc. (US)				
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Matches	89; Conservative	0;	Mismatches	32;	Indels 0; Gaps 0;
OY	13	AAAACTAGATCTATTATTGACGCGCGCCGCAATGGATGCCCGGCGTCAGAGAT	72		
Db	134	AACAGTTAAATTACACTCGCGCCGCTTAAGAACTAGTGGATTCGCCGCGCAGGAAAC	75		
OY	73	TTCGATATCAAGCTTATGATACCGCTGCAGCTCGAGGGGGGCGCTAATCACTAAATTTTGT	132		

DB 74 TCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGCCCGGTACCCAGCTTTGT 15  
OY 133 T 133  
DB 14 T 14

RESULT 9  
AX284796/c 424 bp DNA linear PAT 20-NOV-2001  
LOCUS AX284796  
DEFINITION Sequence 601 from Patent WO0179556.  
ACCESSION AX284796  
VERSION AX284796.1 GI:17045484  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS Lillie, J., Brown, J.L., Bolt, A. and van Huffel, C.  
TITLE Novel genes, compositions and methods for the identification,  
assessment, prevention, and therapy of human cancers  
JOURNAL Patent: WO 0179556-A 601 25-OCT-2001;  
Millennium Predictive Medicine, Inc. (US)  
FEATURES  
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BASE COUNT 87 a 134 c 118 g 85 t  
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Query Match 46.9%; Score 69.4; DB 6; Length 424;  
Best Local Similarity 87.4%; Pred. No. 7e-11;  
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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DB 106 TAGTGGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 47  
OY 107 GGGGGGGCCTACTACTACTAATTGTT 133  
DB 46 GGGGGGGCCTACTACTACTAATTGTT 20

RESULT 10  
AY034154/c 2059 bp DNA circular SYN 23-JUL-2001  
LOCUS AY034154  
DEFINITION Cloning vector pIDM4, complete sequence.  
ACCESSION AY034154  
VERSION AY034154.1 GI:14324126  
KEYWORDS  
SOURCE Cloning vector pIDM4.  
ORGANISM Artificial sequences; vectors.  
REFERENCE  
AUTHORS 1 (bases 1 to 2059)  
TITLE Hamilton, H.L., Schwartz, K.J. and Dillard, J.P.  
Insertion-duplication mutagenesis of neisseria: use in  
characterization of DNA transfer genes in the gonococcal genetic  
island  
JOURNAL J. Bacteriol. 183 (16), 4718-4726 (2001)  
MEDLINE 21359313  
PUBMED 11466274  
REFERENCE 2 (bases 1 to 2059)  
AUTHORS Hamilton, H.L., Schwartz, K.J. and Dillard, J.P.  
TITLE Direct Submission  
JOURNAL Submitted (11-MAY-2001) Medical Microbiology & Immunology,  
University of Wisconsin-Madison, 1300 University Avenue, Madison,  
WI 53706, USA  
FEATURES  
source 1. 2059  
location/Qualifiers  
/organism="Cloning vector pIDM4"  
/db\_xref="taxon:161273"

promoter /note="for insertion-duplication mutagenesis in Neisseria"  
40. .59  
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promoter complement(187. .204)  
/note="r7"  
stem\_loop 277. .311  
gene complement(310. .1113)  
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CDS complement(310. .1044)  
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/db\_xref="GI:14324127"  
/translation="MNEKNIKRSONPITSKHNDIKIMTNIRLNEHDNFEIGSGKH  
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PNIISDILRIKTFDSDIADEIYLIVEGFARKLNLFLMAEVDISLKVPR  
EYFHPKPVNSSLIRLNRRKRSISHRDOKNYFVWKVNRKYKKIFRKNQFNNSLKH  
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RBS complement(1051. .1054)  
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/gene="ermC"  
-35\_signal complement(1108. .1113)  
/gene="ermC"  
misc\_feature 1130. .1139  
/note="DNA uptake sequence (DUS)"  
misc\_feature complement(1145. .1154)  
/note="DNA uptake sequence (DUS)"  
misc\_RNA complement(1276. .1976)  
/note="RNA II"  
rep\_origin complement(1422. .1423)  
-35\_signal 1830. .1835  
-10\_signal 1854. .1859  
misc\_RNA 1866. .1973  
/note="RNA I"  
-10\_signal complement(1984. .1989)  
-35\_signal complement(2007. .2012)  
BASE COUNT 566 a 452 c 424 g 617 t  
ORIGIN

Query Match 46.9%; Score 69.4; DB 12; Length 2059;  
Best Local Similarity 87.4%; Pred. No. 9e-11;  
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 47 TGGTGGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106  
DB 145 TAGTGGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 86  
OY 107 GGGGGGGCCTACTACTACTAATTGTT 133  
DB 85 GGGGGGGCCTACTACTACTAATTGTT 59

RESULT 11  
AB035274 2890 bp mRNA linear PRI 12-JUL-2000  
LOCUS AB035274  
DEFINITION Homo sapiens mRNA for postreplication repair protein hRAD18p.  
ACCESSION AB035274  
VERSION AB035274.1 GI:8960616  
KEYWORDS  
SOURCE Homo sapiens placenta cDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Tateishi, S., Sakuraba, Y., Masuyama, S., Inoue, H. and Yamazumi, M.  
TITLE Dysfunction of human Rad18 results in defective postreplication  
repair and hypersensitivity to multiple mutagens  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7927-7932 (2000)  
MEDLINE 20345089

REFERENCE	2 (bases 1 to 2890)
AUTHORS	Tateishi,S., Yamazumi,M. and Inoue,H.
TITLE	Direct Submission
JOURNAL	Submitted (26-NOV-1999) Satoshi Tateishi, Kumamoto University, Institute of Molecular Embryology; Kihonji 4-24-1, Kumamoto, Kumamoto 862-0976, Japan (E-mail:tate@go.kumamoto-u.ac.jp, Tel:81-096-373-6602, Fax:81-096-373-6604)
FEATURES	Location/Qualifiers
SOURCE	1.2890
gene	/organism="Homo sapiens"
CDS	/db_xref="taxon:9606"
	/chromosome="3"
	/tissue_type="placenta"
	1..2890
	/gene="hRAD18"
	126..1613
	/gene="hRAD18"
	/note="RING-zinc-finger protein"
	/codon_start=1
	/product="postreplication repair protein hRAD18p"
	/protein_id="BA59284.1"
	/db_xref="GI:8980617"
	/translation="MDSLAESRWPBGALVMTIDLLRGICFEPFNIAITIPCCSH
	YCSLIRKFLSKYTCQCPCTCVTPTEPLKNNRIIDELVSLNFRNHLIOLALSPAS
	SPASSSKNNLWAKYTPVPAVSROSLKSGRLMDNFIIRMGSTSELITKEKSKPSP
	KEASPAKTKETRSVEETIAPDPSPAKREPSTSLKQVTVYDPCVGVNIPESHIN
	HLDCSLREKESLRSRVKRRPLKTVNLSDRDILKRLKEGLSTGNKOQLIK
	RHGFVMTNAQCDALHPKSAEIVQETENIEKTRMRLEASKLNEVWVFKDQTEK
	IDELHSYRKRRKSEFQLVDQARKGYKIMGSKQVTVIRKEDSTFKLSSVCMGQ
	DNMSYTFHFSQSKLSDPEELPREDESSCIDIOEVLSSSESDSCSSSDIIRDL
	LEEFAMWASHKNDLOLQTEISPRNNRRRAESAEIERNNRNIN"
BASE COUNT	916 a 585 c 601 g 788 t
ORIGIN	
Query Match	46.9%; Score 69.4; DB 9; Length 2890;
Best Local Similarity	87.4%; Pred. No. 9.5e-11;
Matches	76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
OY	47 TGGTGATCCCCGGGCGCAGGAATTGGATATCAAGCTTATCGATTGACCTGCA 106
Db	2740 TAGTGATCCCCGGGCGCAGGAATTGGATATCAAGCTTATCGATTGACCTGCA 2799
OY	107 GGGGGGCGCTAAGTAATTTTGT 133
Db	2800 GGGGGGCGCGGTACCAAGCTTTGTT 2826
RESULT 12	
AX247548	
LOCUS	AX247548 2958 bp DNA linear PAT 28-SEP-2001
DEFINITION	Sequence 1 from Patent WO0166775.
ACCESSION	AX247548
VERSION	AX247548.1 GI:15862240
KEYWORDS	.
SOURCE	synthetic construct.
ORGANISM	artificial sequences.
REFERENCE	1 (bases 1 to 2958)
AUTHORS	Evans,D.H., Willer,D.O. and Yao,X.D.
TITLE	Dna joining method
JOURNAL	Patent: WO 0166775-A 1 13-SEP-2001;
FEATURES	University of Guelph (CA)
SOURCE	Location/Qualifiers
	1..2958
	/organism="synthetic construct"
	/db_xref="taxon:32630"
	/note="pBM101"
BASE COUNT	748 a 735 c 752 g 723 t
ORIGIN	
Query Match	46.9%; Score 69.4; DB 6; Length 2958;
Best Local Similarity	87.4%; Pred. No. 9.5e-11;
Matches	76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

[illegible]

FEATURES		Location/Qualifiers	
SOURCE		1..2961	
misc_feature		/organism="synthetic construct" /db_xref="taxon:32630"	
BASE COUNT		1..2961 706 a 758 c 735 g 762 t	
ORIGIN			
Query Match	46.9%;	Score 69.4;	DB 12; Length 2961;
Best Local Similarity	87.4%;	Pred. No. 9.5e-11;	
Matches 76;	Conservative 0;	Mismatches 11;	Indels 0; Gaps 0;
OY 47	TGTTGATTCCTCCGGCGTCAGAGATTGATTCAGCTTATCGATTACCGTGCACCTCGA	106	
Db 685	TAGTGGATTCCTCCGGCGTCAGAGATTGATTCAGCTTATCGATTACCGTGCACCTCGA	744	
OY 107	GGGGGGGCGCTTAAGTAACTAATTTTGTT	133	
Db 745	GGGGGGGCGCGGTACCGACTTTGTT	771	

Search completed: November 10, 2002, 06:52:56  
Job time : 721.586 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:42:15 ; Search time 1332 Seconds

(without alignments)  
1799.499 Million cell updates/sec

Title: US-08-935-377-7

Sequence: 1 GGGCAAAATGAAAACTA.....TTGTTTGTGGCCGCCGCC 148

Scoring table: IDENTITY\_NUC

Gap: 10.0 , Gapex: 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: \*  
1: em\_estda:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75.8	51.2	891	14	BQ140386 NF035A10P
2	72.4	48.9	182	13	BQ106115 NL_3_G09
3	72.4	48.9	793	14	BQ143916 BQ143916
4	71.6	48.4	721	17	CNS06DOU AL394084 T7 end of
5	70.4	47.6	682	17	AO074693 CIT-HSP-2
6	70.2	47.4	804	14	BQ158468 BQ158468 NF058H09P

C	7	70	47.3	728	10	AM682547	EST01410
C	8	69.8	47.2	182	13	BQ105962	BQ105962 NL_2_R23
C	9	69.8	47.2	186	13	BQ105965	BQ105965 NL_1_G23
C	10	69.8	47.2	188	17	CNS06X09	AL415375 T7 end of
C	11	69.6	47.0	198	17	CNS06X01	AL419128 T7 end of
C	12	69.4	46.9	162	10	BE428068	BE428068 MTD002.H1
C	13	69.4	46.9	390	9	AU234451	AU234451 AU234451
C	14	69.4	46.9	400	9	AU278852	AU278852 AU278852
C	15	69.4	46.9	914	17	AO937400	AO937400 NB2-011 H
C	16	69.4	46.9	912	17	CNS06U55	AL415767 T7 end of
C	17	69.2	46.8	175	13	BQ106167	BQ106167 NL_3_108
C	18	69.2	46.8	182	13	BQ106149	BQ106149 NL_3_107
C	19	69.2	46.8	182	13	BQ106159	BQ106159 NL_3_122
C	20	69.2	46.8	182	13	BQ106178	BQ106178 NL_3_K05
C	21	69.2	46.8	182	13	BQ106180	BQ106180 NL_3_K07
C	22	69.2	46.8	757	14	BQ155148	BQ155148 NF076G11T
C	23	68.8	46.5	674	10	AV681474	AV681474 AV681474
C	24	68.8	46.5	776	10	AV681505	AV681505 AV681505
C	25	68.8	46.5	786	10	AV681504	AV681504 AV681504
C	26	68.8	46.5	802	10	AV681486	AV681486 AV681486
C	27	68.8	46.5	806	10	AV681464	AV681464 AV681464
C	28	68.8	46.5	818	17	CNS06URU	AL416224 T7 end of
C	29	68.4	46.2	295	10	BE428455	BE428455 MTD007.CO
C	30	68.4	46.2	608	17	AQ009167	AQ009167 CIT-HSP-2
C	31	68.2	46.1	829	17	AO937397	AO937397 NB2-006 H
C	32	68.2	45.9	928	17	CNS06W2E	AL417900 T7 end of
C	33	67.8	45.8	528	17	BQ6968	BQ6968 CIT978SK-A-
C	34	67.6	45.7	107	13	BM398556	BM398556 5009-0-47
C	35	67.6	45.7	211	17	CNS06CB9	AL392299 T7 end of
C	36	67.4	45.5	108	17	BE492551	BE492551 WHE0554.C
C	37	67.4	45.5	108	17	BE4292	BE4292 CIT-HSP-201
C	38	67.4	45.5	124	10	AM914179	AM914179 EST345483
C	39	67.4	45.5	128	17	CNS07GJ4	AL609826 Anophiles
C	40	67.4	45.5	141	9	AU037147	AU037147 AU037147
C	41	67.4	45.5	141	17	B95279	B95279 CIT-HSP-217
C	42	67.4	45.5	144	17	B80294	B80294 CIT-HSP-204
C	43	67.4	45.5	157	12	BR281431	BR281431 EST446022
C	44	67.4	45.5	169	13	BQ106719	BQ106719 NL_5_N23
C	45	67.4	45.5	169	17	AQ013255	AQ013255 CIT-HSP-2

#### ALIGNMENTS

RESULT 1  
BQ140386 891 bp mRNA linear EST 26-APR-2002  
LOCUS NF035A10PH1F1081 Phoma-infected Medicago truncatula CDNA clone  
DEFINITION NF035A10PH 5', mRNA sequence.  
ACCESSION BQ140386  
VERSION BQ140386.1 GI:20276512  
KEYWORDS  
SOURCE  
ORGANISM  
barrel medic.  
Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
Medicago.  
1 (bases 1 to 891)  
REFERENCE  
AUTHORS Watson,B.S., Shih,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,  
Gonzales,R.A., Bell,C.J., Imman,D.T., Maugh,M.E., Sullivan,J.P.,  
May,G.D. and Paiva,N.L.  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
Medicago truncatula Phoma-infected library  
Unpublished (2002)  
Contact: Paiva N.  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7317  
Fax: 580 221 7380  
Email: nlpaiva@noble.org  
Insert Length: 891 Std Error: 0.00

TITLE  
JOURNAL  
COMMENT



```

Db      83 TAGTGATGATCCCCGGGCTCAGGAATTCGATATCAAGCTTATGATACCGTGACCTCGA 142
Qy      107 GGGGGGGCCCTAACTAACTAATT 128
Db      143 GGGGGGGGGCCGAGTACCAAT 164

RESULT 4
LOCUS   CENS06D0U                               721 bp    DNA       linear   GSS 05-APR-2001
DEFINITION T7 end of clone AR0AA014H10 of library AR0AA from strain CBS 732 of
ACCESSION Zygosacharomyces rouxii, genomic survey sequence.
VERSION    AL394084
KEYWORDS   AL394084.1 GI:12144845
SOURCE     GSS; clone AR0AA014H10; RST AR0AA014H10CPL.
ORGANISM   Zygosacharomyces rouxii.
           Zygosacharomyces rouxii.
           Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
           Saccharomycetales; Saccharomycetaceae; Zygosacharomyces.
REFERENCE 1 (bases 1 to 721)
AUTHORS   Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
           Boitlin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,
           de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
           Malpertuy,A., Neugeglise,C., Ozler-Kalogeropoulos,O., Potier,S.,
           Saurin,M., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
           Winkler,P. and Weissenbach,J.
           Genomic exploration of the hemiascomycetous yeasts: 1. A set of
           yeast species for molecular evolution studies
           FEBS Lett. 487 (1), 3-12 (2000)
JOURNAL   MEDLINE
PUBMED    20584711
TITLE     2 (bases 1 to 721)
AUTHORS   de Montigny,J., Straub,M., Potier,S., Tekala,F., Dujon,B.,
           Winkler,P., Artiguenave,F. and Souciet,J.
           Genomic exploration of the hemiascomycetous yeasts: 8.
           Zygosacharomyces rouxii
           FEBS Lett. 487 (1), 52-55 (2000)
JOURNAL   MEDLINE
PUBMED    20584718
TITLE     3 (bases 1 to 721)
AUTHORS   Genoscope.
           Direct Submission
           Submitted (28-MAR-2001) Genoscope - Centre National de Sequencage,
           2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
           sequef@genoscope.cns.fr Web : www.genoscope.cns.fr)
           This BAC end sequence is part of a random genomic sequencing
           program of thirteen yeast species:
           . Saccharomyces bayanus var. uvarum,
           . Saccharomyces exiguus,
           . Saccharomyces servazii,
           . Zygosacharomyces rouxii,
           . Saccharomyces kluyveri,
           . Kluyveromyces thermotolerans,
           . Kluyveromyces lactis var. lactis,
           . Kluyveromyces marxianus var. marxianus
           . Pichia angusta,
           . Debaryomyces hansenii var. hansenii,
           . Pichia sorbitophila,
           . Candida tropicalis and
           . Yarrowia lipolytica.
           Genomic inserts of 3 to 5 kb were prepared and both extremities
           were sequenced. See keywords for description of this sequence and
           for the sequence of the other extremity of this insert.
FEATURES
source    Location/Qualifiers
           1..721
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           /strain="CBS 732"
           /db_xref="taxon:4956"
           /clone="AR0AA014H10"
           /clone_1db="AR0AA"
           /note="end : T7"

BASE COUNT      188 a      100 c      201 g      193 t      39 others

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ORIGIN
Query Match      48.4%; Score 71.6; DB 17; Length 721;
Best Local Similarity 81.4%; Pred. No. 8.4e-13;
Matches 83; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy      14 AAAACTGATCTATTATTCGACGCGGCCCGCATGATGATGATCCCCGGGCTCAGCAATT 73
Db      215 ATACTTATGATGTTTATTATCCATGATAGCCAGCTGATCCCGGCTGCAGCAATT 274

Qy      74 CGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCC 115
Db      275 CGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCC 316

RESULT 5
LOCUS   AO074693/c                               682 bp    DNA       linear   GSS 20-AUG-1998
DEFINITION CTT-HSP-2301L23.TF CTT-HSP Homo sapiens genomic clone 2301L23, DNA
ACCESSION AO074693
KEYWORDS   AO074693.1 GI:3436811
SOURCE     GSS.
ORGANISM   human.
           Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 682)
AUTHORS   Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
           Berry,K., Granger,D., Sub,E., Wible,C., Shizuya,H., Simon,M. and
           Venter,J.C.
           Use of a random human BAC End Sequence Database for Sequence-Ready
           Map Building
           Unpublished (1998)
           Contact: Mark Adams
           Department of Eukaryotic Genomics
           The Institute for Genomic Research
           9712 Medical Center Dr., Rockville, MD 20850, USA
           Tel: 301 838 0200
           Fax: 301 838 0208
           Email: mdamas@tigr.org
           Clones are available from Research Genetics (info@resgen.com). BAC
           end search page:
           http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.
           Seq primer: M13-21
           Class: BAC ends.
FEATURES
source    Location/Qualifiers
           1..682
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           /db_xref="taxon:9606"
           /clone="2301L23"
           /clone_1db="CTT-HSP"
           /sex="Male"
           /cell_type="Sperm"
           /note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
           HindIII"

BASE COUNT      156 a      187 c      187 g      151 t      1 others

Query Match      47.6%; Score 70.4; DB 17; Length 682;
Best Local Similarity 92.5%; Pred. No. 2.1e-12;
Matches 74; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      47 TGGTGAATCCCCGGGCTGACGGAATTCGATATCAAGCTTATGATACCGTCGACCTCGA 106
Db      80 TAGTGATGATCCCCGGGCTGACGGAATTCGATATCAAGCTTATGATACCGTCGACCTCGA 21

Qy      107 GGGGGGGCCCTAACTAACTAA 126
Db      20 GGGGGGGGGCCGAGTACCA 1

RESULT 6

```

LOCUS	804 bp	mRNA	linear	EST 24-APR-2002
DEFINITION	B0158468 NF058H09PL1078 Phosphate starved leaf Medicago truncatula cDNA clone NF058H09PL 5', mRNA sequence.			
ACCESSION	B0158468			
VERSION	B0158468.1 GI:20295525			
KEYWORDS	EST.			
SOURCE	barrel medic.			
ORGANISM	Medicago truncatula			
REFERENCE	Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.			
AUTHORS	Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Jman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.			
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Harrison MJ Plant Biology Division The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7325 Fax: 580 221 7380 Email: mjharrison@noble.org Insert Length: 804 Std Error: 0.00 Plate: 058 row: H column: 09 Seq primer: TCACACAGGAACACGATGAC. Location/Qualifiers 1..804 /organism="Medicago truncatula" /db_xref="taxon:3880" /clone="NF058H09PL" /clone_id="phosphate starved leaf" /tissue_type="leaf" /dev_stage="trifoliolate" /note="Vector: lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20um potassium phosphate. RNA was prepared from above ground tissues." 215 a 202 c 181 g 165 t 41 others			
BASE COUNT	215 a 202 c 181 g 165 t 41 others			
ORIGIN	1..804			
Query Match	47.4%	Score 70.2;	DB 14;	Length 804;
Best Local Similarity	88.2%;	Freq. No. 2,4e-12;		
Matches	75;	Conservative 0;	Mismatches 10;	Indels 0;
Gaps	0;			
QY	47 TGGTGATGCCCGGGGCTGCAGAGATTGCATTCAGCTTATTCGATTCGCTGACCTCGA	106		
DB	80 TAGTGGATGCCCGGGGCTGCAGAGATTGCATTCAGCTTATTCGATTCGCTGACCTCGA	139		
QY	107 GGGGGGGCCCTAAGTAATTTTG	131		
DB	140 GGGGGGGCCCTGTAACCAATTCG	164		
RESULT 7	AM682547/c 728 bp mRNA linear EST 14-APR-2000			
LOCUS	AM682547			
DEFINITION	EST01410 E8.5 mouse craniofacial subregion cDNA library Mus musculus cDNA clone e064, mRNA sequence.			
ACCESSION	AM682547			
VERSION	AM682547.1 GI:7557255			
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia, Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 728)			
AUTHORS	Mushkaml,Y., Li,H., Chowdhury,S., Yamada,K.M. and Yamada,Y.			

JOURNAL COMMENT	EST sequences from E8.5 mouse craniofacial cDNA library Unpublished (2000) Contact: Yoshihiko Yamada Craniofacial Developmental Biology and Regeneration Branch National Institute of Dental and Craniofacial Research 9000 Rockville Pike, Building 30, Room 405, NIDCR, NIH, Bethesda, MD 20892 Tel: 301 496 2111 Fax: 301 402 0897 Email: yoshi.yamada@nih.gov Seq primer: M13 reverse					
FEATURES	Location/Qualifiers					
source	1 . -728 /organism="Mus musculus" /strain="ICR" /db_xref="taxon:10090" /clone="e064" /clone_lib="E8.5 mouse craniofacial subtraction cDNA library" /tissue_type="craniofacial tissues" /dev_stage="embryonic day 8.5" /note="Vector: pT-Adv; A subtraction cDNA library was constructed from E8.5 mouse craniofacial mRNA subtracted from EL3.5 mouse craniofacial mRNA."					
BASE COUNT	191 a 158 c 179 g 188 t 12 others					
ORIGIN						
Query Match	47.3%; Score 70; DB 10; Length 728;					
Best Local Similarity	80.4%; Pred. No. 2.8e-12;					
Matches	82; Conservative 0; Mismatches 20; Indels 0; Gaps 0.					
CY	42	CGCCATGTTGGATTCCCCCGGGCTGCAGGAATTCGATTCACGCTTATCGATTCAGTCGCAC	101			
Db	117	CTCGAGGCGCGAATCCCCGSGCTGCAGGAATTCGATTCACGCTTATCGATTCACCGTGCAC	58			
OY	102	CTCGAGGGGGGGGCCCTAACTAATAATTTTTGTTTTGCGGCC	143			
Db	57	CTCGAGGGGGGGCCCGGTAACCACCAATTCGCCCTATAGTGGGCC	16			
RESULT 8						
BI305962/c	182 bp mRNA linear EST 20-JUL-2000					
LOCUS	NL_2_K23 Drought stress (leaf) Oryza sativa cDNA clone NL_2_K23 3'					
DEFINITION	mRNA sequence.					
ACCESSION	BI305962					
VERSION	BI305962.1 GI:14981284					
KEYWORDS	EST.					
SOURCE	Oryza sativa.					
ORGANISM	Oryza sativa					
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ephartriodeae; Oryzaceae; Oryza.					
AUTHORS	1 (bases 1 to 182) Reddy,A.R., Ramakrishna,W., Chandrasekhar,A., Nagabushan,I., Ravindrababu,P. and Bennetzen,J.L. Novel EST enrichment with normalized cDNA libraries from drought stressed rice (Oryza sativa L.cv Nagina 22)					
TITLE	Unpublished (2001)					
JOURNAL	Contact: Reddy AR					
COMMENT	Department of Plant Sciences, School of Life Sciences University of Hyderabad P.O. Central University, Hyderabad-500 046, A.P, India Tel: 0091-40-3010265 Fax: 0091-40-3010145 Email: arjunsleubhd.ernet.in Insert Length: 182 Std Error: 0.00 Plate: 2 row: K column: 23 Seq primer: GTAACAAGCAGCGCACGTG. location/Qualifiers 1 . 182 /organism="Oryza sativa" /cultivar="Nagina 22 (indica sub sp)"					



		/db_xref="taxon:4530"	
		/clone="NL_2_K23"	
		/clone_lib="Drought stress (leaf)"	
		/tissue_type="Entire leaf tissue"	
		/dev_stage="35 day-old seedlings"	
		/note="Organ: leaf; Vector: T73Pac; ESTs from normalized leaf cDNA library from drought stressed seedlings"	
BASE COUNT		34 a	48 c 52 g 46 t 2 others
ORIGIN			
Query Match			
Best Local Similarity		47.2%;	Score 69.8; DB 13; Length 182;
Matches 74; Conservative		0;	Pred. No. 3.4e-12; Mismatches 8; Indels 0; Gaps 0;
OY	47	TGGTGATATCCCCGGGGCGCAGAGATTGCATATCAAGCTTATCAGTATACCGTGCAGCTCGA	106
DB	109	TATGTGATATCCCCGGGGCGCAGAGATTGCATATCAAGCTTATCAGTATACCGTGCAGCTCGA	50
OY	107	GGGGGGGCTTACTACTAATAT 128	
DB	49	GGGGGGGCGCCGTCACCAAT 28	
RESULT 9			
BI305695/c		186 bp	mRNA linear EST 20-JUL-2001
LOCUS		NL_1_G23 Drought stress (leaf)	Oryza sativa cDNA clone NL_1_G23 3'
DEFINITION		mRNA sequence.	
ACCESSION		BI305695	
VERSION		BI305695.1	GI:14981017
KEYWORDS		EST.	
SOURCE		Oryza sativa.	
ORGANISM		Oryza sativa	
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
		Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
		Ehrhartoideae; Oryzaceae; Oryza.	
		1 (bases 1 to 186)	
REFERENCE		Reddy,A.R., Ramakrishna,W., Chandrasekhar,A., Nagabhushan,I.,	
AUTHORS		Ravindrababu,P. and Bennetzen,J.L.	
		Novel EST enrichment with normalized cDNA libraries from drought	
		stressed rice (Oryza sativa L.cv Nagina 22)	
		unpublished (2001)	
JOURNAL		Contact: Reddy AR	
COMMENT		Department of Plant Sciences, School of Life Sciences	
		University of Hyderabad	
		P.O. Central University, Hyderabad-500 046, A.P., India	
		Tel: 0091-40-3010265	
		Fax: 0091-40-3010145	
		Email: arjuls@uohyd.ernet.in	
		Insert length: 186 Std Error: 0.00	
		Plate: 1 row: G column: 23	
		Seq primer: GTAACGACGCGCAGTC.	
FEATURES		Location/Qualifiers	
source		1..186	
		/organism="Oryza sativa"	
		/cultivar="Nagina 22 (Indica sub sp)"	
		/db_xref="taxon:4530"	
		/clone="NL_1_G23"	
		/clone_lib="Drought stress (leaf)"	
		/tissue_type="Entire leaf tissue"	
		/dev_stage="35 day-old seedlings"	
		/note="Organ: leaf; Vector: T73Pac; ESTs from normalized leaf cDNA library from drought stressed seedlings"	
BASE COUNT		35 a	47 c 56 g 46 t 2 others
ORIGIN			
Query Match			
Best Local Similarity		47.2%;	Score 69.8; DB 13; Length 186;
Matches 74; Conservative		0;	Pred. No. 3.4e-12; Mismatches 8; Indels 0; Gaps 0;
OY	47	TGGTGATATCCCCGGGGCGCAGAGATTGCATATCAAGCTTATCAGTATACCGTGCAGCTCGA	106
DB	113	TATGTGATATCCCCGGGGCGCAGAGATTGCATATCAAGCTTATCAGTATACCGTGCAGCTCGA	54

Oy	107	GGGCGGCCCTACTACATAATT	128
Dd	53	GGGCGGCNCCCGTACCATT	32
RESULT 10	CNS06U49	188 bp	DNA linear GSS 05-JUL-2001
LOCUS	CNS06U49	T7 end of clone AX0AA004H12 of library AX0A from strain CBS 7064	
DEFINITION	of Pichia farinosa, genomic survey sequence.		
ACCESSION	AL15375		
VERSION	AL15375.1	GI:12194520	GSS.
KEYWORDS	Pichia farinosa.		
SOURCE	Pichia farinosa.		
ORGANISM	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces;		
REFERENCE	Saccharomycetales; Saccharomycetaceae; Pichia.		
AUTHORS	Souciety,J.L., Aigle,M., Artiguenave,F., Blandin,G., Boitoin-Pikunara,M., Bon,E., Brottier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Lorente,B., Maupertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potler,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Wesoloski-Louvel,M., Wincker,P. and Weissenbach,J.		
JOURNAL MEDLINE	Genomic exploration of the hemiascomycetous yeasts : 1. A set of yeast species for molecular evolution studies FEBS Lett. 487 (1), 3-12 (2000)		
PUBLISHED	20584711		
AUTHORS	2 (bases 1 to 188) de Montigny,J., Spehner,C., Souciety,J., Tekala,F., Dujon,B., Wincker,P., Artiguenave,F. and Potler,S. Genomic exploration of the hemiascomycetous yeasts : 15. Pichia sorbitophila FEBS Lett. 487 (1), 87-90 (2000)		
JOURNAL MEDLINE	20584725		
PUBLISHED	1152890		
REFERENCE	3 (bases 1 to 188) Genoscope.		
TITLE	Direct Submission Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, rue Gaston Cremlieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)		
JOURNAL TITLE	This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii, Lactariomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.		
COMMENT	Location/Qualifiers 1..188 /organism="Pichia farinosa" /strain="CBS 7064" /db_xref="taxon:4920" /clone="AX0AA004H12" /clone_1id="AX0AA" /note="end : T7"		
FEATURES	source		
BASE COUNT	48 a	40 c	59 g
ORIGIN	40 t	1 others	
Query Match	47.2%; Score 69.8;	DB 17;	Length 188;
Best Local Similarity	91.4%;	Pred. No. 3,4e-12;	
Matches	74;	Conservative 0;	Mismatches 7;
		Indels 0;	Gaps 0;
Oy	35	ACGCGCGCAGCATGGTGGATCCCCGGGCTCAGAGAATTCATATCAAGCTTATCGATAC	94
Dd	75	AGGAGGCGCAAAGATGATCCCGGGCTCACAGGAATTCATATCAAGCTTATCGATAC	134

RESULT	11
CNS06X01	198 bp DNA linear GSS 06-JUL-2001
LOCUS	77 end of clone AX0AA037A11 of library AX0AA from strain CBS 7064
DEFINITION	of <i>Pichia farinosa</i> , genomic survey sequence.
ACCESSION	AL419128
VERSION	AL419128.1 GI:12202306
KEYWORDS	GSS.
SOURCE	<i>Pichia farinosa</i> .
ORGANISM	<i>Pichia farinosa</i> .
REFERENCE	Eukaryote; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; <i>Pichia</i> .
AUTHORS	1 (bases 1 to 198) Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Boitron-Pukhara,M., Bon,E., Brotier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Lorente,B., Malpertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,M., Tekala,F., Toftano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
TITLE	Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
JOURNAL	FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE	20584711
PUBMED	11152876
REFERENCE	2 (bases 1 to 198) de Montigny,J., Spehner,C., Souciet,J., Tekala,F., Dujon,B., Wincker,P., Artiguenave,F. and Potier,S.
AUTHORS	Genomic exploration of the hemiascomycetous yeasts: 15. <i>Pichia sorbitophila</i>
TITLE	FEBS Lett. 487 (1), 87-90 (2000)
JOURNAL	20584725
MEDLINE	11152890
PUBMED	3 (bases 1 to 198)
REFERENCE	Genoscope.
AUTHORS	Direct Submission
TITLE	Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)
JOURNAL	This GSS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>uvaurum</i> , <i>Saccharomyces exiguus</i> , <i>Saccharomyces servazzii</i> , <i>Zygosaccharomyces rouxii</i> , <i>Saccharomyces kluyveri</i> , <i>Kluyveromyces thermotolerans</i> , <i>Kluyveromyces lactis</i> var. <i>lactis</i> , <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> , <i>Pichia angusta</i> , <i>Debaryomyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
COMMENT	Location/Qualifiers
FEATURES	1..198
SOURCE	/organism="Pichia farinosa" /strain="CBS 7064" /db_xref="taxon:4920" /clone="AX0AA037A11" /clone_lib="AX0AA" /note="end : 177"
BASE COUNT	42 a 59 c 54 g 41 t 2 others
ORIGIN	
Query Match	47.0%; Score 69.6; DB 17; Length 198;
Best Local Similarity	94.7%; Pred. No. 3.9e-12;
Matches	72; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
40	GGCGCATGGTGGATCCCGGGCTGCAGAAATTCGATATCAAGCTTATGATACCGTGC 99
111	
104	GGCTTCAAGCTGGATCCCGGGCTGCAGAAATTCGATATCAAGCTTATGATACCGTGC 163
100	ACCTGAGGGGGGGGCC 115

Db	164	ACCTCGAGGGGGGCC	179	
RESULT 12				
LOCUS	BE428068			
DEFINITION	MD0002.H10F990615	ITEC	MTD durum wheat Root Library	Trilicium
ACCESSION	BE428068			
VERSION	BE428068.1	GI:9425911		
KEYWORDS	EST.			
SOURCE	durum wheat.			
ORGANISM	Trilicium turgidum subsp. durum			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae			
	; Triliceae; Trilicium.			
REFERENCE	1	(bases 1 to 162)		
AUTHORS	Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier			
	S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,			
	Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,			
	Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,			
	Pechion,I.N., Quilset,C., Schuch,W., Selvaraj,G., Sharillou,M.,			
	Sorells,M., Warburton,M. and Wenzel,G.			
TITLE	International Triliceae EST Cooperative (ITEC): Production of			
	Expressed Sequence Tags for Species of the Triliceae			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Joudrier P			
	INRA, Unite de Biochimie et Biologie Moleculaire des Cereales			
	2, place VIALA, 34060 Montpellier cedex 01 FRANCE			
	Tel: 33 4 99 61 23 84			
	Fax: 33 4 99 61 23 48			
	Email: joudrier@enscm.inra.fr			
	International Triliceae EST Cooperative (ITEC)			
	http://wheat.pw.usda.gov/genome.			
FEATURES				
source	1. 162			
	/organism="Trilicium turgidum subsp. durum"			
	/cultivar="Siliana"			
	/db_xref="taxon:4567"			
	/clone="MTD002.H10"			
	/clone_lib="ITEC MTD Durum Wheat Root Library"			
	/tissue_type="root"			
	/dev_stage="3-day-old seedling, water-stressed"			
	/note="vector: pSPORT1; T7 primers used. See pSPORT1			
	polylinker site. 0.3-2.0 kbp average insert size."			
BASE COUNT	28 a 42 c 49 g 43 t			
ORIGIN				
Query Match	46.9%;	Score 69.4;	DB 10;	Length 162;
Best Local Similarity	87.4%;	Pred. No. 4.6e-12;		
Matches	76;	Conservative	0;	Mismatches 11;
			Indels	0;
			Gaps	0;
QY	47	TGCGATGATCCCCGGGCGCAGAGTTCGATTCAGCTTATCGATTACCGTCGACCTCGA	106	
Db	22	TAGTGATGATCCCCGGGCGTCGACGATTCGATTCAGCTTATCGATTACCGTCGACCTCGA	81	
QY	107	GGGGGGGCCCTAAGTAACTAATTTGTT	133	
Db	82	GGGGGGGCCCTAAGTAACTAATTTGTT	108	
RESULT 13				
LOCUS	AU234451			
DEFINITION	AU234451	Bovine placenta cDNA	Bos taurus cDNA clone	Clin153 3'
ACCESSION	AU234451			
VERSION	AU234451.1	GI:15719669		
KEYWORDS	EST.			
SOURCE	cow.			
ORGANISM	Bos taurus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			



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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 04:19:15 ; Search time 174.627 Seconds

(without alignments)  
1908.619 Million cell updates/sec

Title: US-08-935-377-7

Perfect score: 148

Sequence: 1 GGCCAAAATGTGAAAACTA.....TTGTTTGTGGCCGCCGCC 148

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*

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4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*

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23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*

24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	148	100.0	148	21	AAA15236
2	148	100.0	148	22	ABA01477
3	148	100.0	148	24	AAD31779
4	137	92.6	149	21	AAA15237
5	137	92.6	149	22	ABA01478
6	137	92.6	149	24	AAD31780
7	136	91.9	150	21	AAA15238
8	136	91.9	150	22	ABA01479
9	136	91.9	150	24	AAD31781

10	132	89.2	145	21	AAA15235	Nucleotide sequenc
11	132	89.2	145	22	ABA01476	Partial p7.5/ATG1/
12	132	89.2	145	24	AAD31778	Modified p7.5/tk v
13	77	52.0	638	23	ABV44137	Human prostate exp
14	76.8	51.9	658	23	ABV42450	Human prostate exp
15	76.8	51.9	671	23	ABV41330	Human prostate exp
16	76.2	51.5	467	23	ABV45888	Human prostate exp
17	75.6	51.1	408	23	ABV35567	Human prostate exp
18	75.6	51.1	410	23	ABV32098	Human prostate exp
19	75.6	51.1	410	23	ABV41036	Human prostate exp
20	75.6	51.1	436	23	ABV38427	Human prostate exp
21	75.6	51.1	536	23	ABV38679	Human prostate exp
22	75.2	50.8	611	23	ABV42990	Human prostate exp
23	75.2	50.8	612	23	ABV34128	Human prostate exp
24	75.2	50.7	685	23	ABV35296	Human prostate exp
25	75	50.7	685	23	ABV42445	Human prostate exp
26	75	50.7	685	23	ABV44131	Human prostate exp
27	74.8	50.5	483	23	ABV36363	Human prostate exp
28	74.8	50.5	483	23	ABV45392	Human prostate exp
29	74.8	50.5	615	23	ABV32092	Human prostate exp
30	74.6	50.4	372	23	ABV43508	Human prostate exp
31	74.6	50.4	435	23	ABV36241	Human prostate exp
32	74.6	50.4	435	23	ABV45283	Human prostate exp
33	74.6	50.4	450	23	ABV38398	Human prostate exp
34	74.6	50.4	460	23	ABV33323	Human prostate exp
35	74.6	50.4	460	23	ABV42246	Human prostate exp
36	74.6	50.4	469	23	ABV42812	Human prostate exp
37	74.6	50.4	528	23	ABV38626	Human prostate exp
38	74.6	50.4	573	23	ABV38615	Human prostate exp
39	74.4	50.3	431	23	ABV36186	Human prostate exp
40	74.2	50.1	437	23	ABV38437	Human prostate exp
41	74.2	50.1	459	23	ABV31199	Human prostate exp
42	74.2	50.1	499	23	ABV40169	Human prostate exp
43	73.8	49.9	555	23	ABV38249	Human prostate exp
44	73.6	49.7	405	23	ABV35439	Human prostate exp
45	73.6	49.7	405	23	ABV44267	Human prostate exp

#### ALIGNMENTS

RESULT 1

ID AAA15236 standard; DNM: 148 BP.

XX

AC AAA15236:

XX

DT 04-SEP-2000 (first entry)

XX

DE Nucleotide sequence of a fragment of the plasmid p7.5/ATG1/tk.

XX

KW Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;

KW vaccine; tumour regression; cancer; infection; ss.

XX

OS Synthetic.

XX

PN WO200028016-A1.

XX

PD 18-MAY-2000.

XX

PE 10-NOV-1998; 98WO-US24029.

XX

PR 10-NOV-1998; 98WO-US24029.

XX

PA (UVRP) UNIV ROCHESTER.

XX

PI Zauderer M;

XX

DR WPI; 2000-376533/32.

XX

PT Novel method of identifying target epitopes or antigens specific for

PT human tumors, cancers and infected cells involving screening expression

PT library products of a cell expressing the target epitope

```
XX PS Disclosure; Fig 2; 132pp; English.
XX CC The present sequence represents a fragment of a vaccinia transfer
CC CC plasmid, which is used in the course of the invention. The
CC CC specification describes a method for identifying a target epitope.
CC CC The method comprises screening the products of an expression library
CC CC from a cell expressing the target epitope with cytotoxic T cells
CC CC generated against the cell to identify DNA clones expressing the target
CC CC epitope. The method may also comprise providing a cytotoxic T cell
CC CC specific for a gene product differentially expressed by a cell and
CC CC measuring the cross-reactivity of the cytotoxic T cell. The methods are
CC CC useful for identifying tumour specific target epitopes and antigens which
CC CC are useful in immunogenic compositions or vaccines to induce the
CC CC regression of tumors, cancers or infections in mammals. The genes
CC CC expressed in a panel of tumour cells that are derived from single
CC CC immortalised, non-tumorigenic cell line are used to generate HLA
CC CC restricted cytotoxic T cells which are evaluated for activity against
CC CC tumour cells. The method is useful to identify potential antigens
CC CC expressed not only by the pathogen but also by the host cells whose gene
CC CC expression is altered as a result of infection. The differential gene
CC CC expression strategies can be applied to identify immunogenic molecules
CC CC of cells infected with virus, fungus or mycobacterium.
XX SQ Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;
XX
XX Query Match 100.0%; Score 148; DB 21; Length 148;
XX Best Local Similarity 100.0%; Pred. No. 2.5e-41;
XX Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCCAAAATGAAAACTAGATCTATTATTGACGCGCGGCCCATGTGATCCCGC 60
DB 1 GGGCCAAAATGAAAACTAGATCTATTATTGACGCGCGGCCCATGTGATCCCGC 60
QY 61 GGGTCGAGAAATTCGATATCAAGCTTATCCATACCGTCGACCTGAGGGGGGCTTACT 120
DB 61 GGGTCGAGAAATTCGATATCAAGCTTATCCATACCGTCGACCTGAGGGGGGCTTACT 120
QY 121 AACTAATTTGTTTGTGGGCGCGGCC 148
DB 121 AACTAATTTGTTTGTGGGCGCGGCC 148
XX
XX RESULT 2
XX ABA01477
XX ID ABA01477 standard; DNA; 148 BP.
XX AC ABA01477;
XX XX
XX DT 04-FEB-2002 (first entry)
XX DE Partial p7.5/ATG1/Lk sequence.
XX XX
XX KW Cell death; toxic gene; tumour suppressor; ds.
XX OS Synthetic.
XX XX
XX PN W0200172995-A2.
XX XX
XX PD 04-OCT-2001.
XX XX
XX PF 28-MAR-2001; 2001WO-US09953.
XX XX
XX PR 28-MAR-2000; 2000US-0192586.
XX PR 10-MAY-2000; 2000US-0203343.
XX PR 23-JAN-2001; 2001US-0263226.
XX PR 27-FEB-2001; 2001US-0271426.
XX XX
XX PA (UVRP ) UNIV ROCHESTER.
XX XX
XX PI Zauderer M, Smith ES;
XX DR WPI; 2001-570897/64.
```

```
XX XX Selecting target polynucleotides, particularly toxic genes, involves
XX PT introducing a library of insert polynucleotides into a host cell
XX PT population, where the target polynucleotide promotes cell death -
XX PS Disclosure; Fig 8; 359pp; English.
XX XX
XX CC The present invention relates to a method for selecting a target
XX CC polynucleotide. The method comprises introducing into a host cell
XX CC population a library of insert polynucleotides, where expression of the
XX CC target polynucleotide directly or indirectly promotes host cell death.
XX CC The cells are cultured and the insert polynucleotides are collected from
XX CC the cells which die. The method is useful for selecting target
XX CC polynucleotides, particularly polynucleotides which alter cell phenotypes
XX CC of induce or inhibit cell death. The method can be used to isolate toxic
XX CC genes such as tumour suppressors. The present sequence was used to
XX CC illustrate the method of the present invention.
XX SQ Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;
XX
XX Query Match 100.0%; Score 148; DB 22; Length 148;
XX Best Local Similarity 100.0%; Pred. No. 2.5e-41;
XX Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCCAAAATGAAAACTAGATCTATTATTGACGCGCGGCCCATGTGATCCCGC 60
DB 1 GGGCCAAAATGAAAACTAGATCTATTATTGACGCGCGGCCCATGTGATCCCGC 60
QY 61 GGGTCGAGAAATTCGATATCAAGCTTATCCATACCGTCGACCTGAGGGGGGCTTACT 120
DB 61 GGGTCGAGAAATTCGATATCAAGCTTATCCATACCGTCGACCTGAGGGGGGCTTACT 120
QY 121 AACTAATTTGTTTGTGGGCGCGGCC 148
DB 121 AACTAATTTGTTTGTGGGCGCGGCC 148
XX
XX RESULT 3
XX AAD31779
XX ID AAD31779 standard; DNA; 148 BP.
XX AC AAD31779;
XX XX
XX DT 18-JUN-2002 (first entry)
XX DE Modified p7.5/Lk vector, p7.5/ATG1/Lk.
XX XX
XX KW Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
XX KW vaccine; immune response; cytostatic; p7.5/Lk vector; thymidine kinase;
XX KW p7.5/ATG1/Lk vector; ds.
XX OS Vaccinia virus.
XX XX
XX FH Key
XX FH Location/Qualifiers
XX FT misc_signal
XX FT /tag= a
XX FT /note= "Translation start codon"
XX FT 116..118
XX FT /tag= b
XX FT /note= "Translation stop codon"
XX FT 120..122
XX FT /tag= c
XX FT /note= "Translation stop codon"
XX FT 124..126
XX FT /tag= d
XX FT /note= "Translation stop codon"
XX FT 132..138
XX FT /tag= e
XX FT /note= "Transcription stop signal"
XX PN US2002018785-A1.
XX XX
```



```

XX Cell death; toxic gene; tumour suppressor; ds.
KW Synthetic.
XX
XX WO200172995-A2.
XX
XX 04-OCT-2001.
XX
XX 28-MAR-2001; 2001WO-US09953.
XX
XX 28-MAR-2000; 2000US-0192586.
PR 10-MAY-2000; 2000US-0203343.
PR 23-JAN-2001; 2001US-0263226.
PR 27-FEB-2001; 2001US-0271426.
XX
XX (UVRP ) UNIV ROCHESTER.
XX
XX Zauderer M, Smith ES;
XX
XX WPI; 2001-570897/64.
XX
XX Selecting target polynucleotides, particularly toxic genes, involves
PT introducing a library of insert polynucleotides into a host cell
PT population, where the target polynucleotide promotes cell death -
XX
XX Disclosure; Fig 8; 359pp; English.
XX
XX The present invention relates to a method for selecting a target
CC polynucleotide. The method comprises introducing into a host cell
CC a population a library of insert polynucleotides, where expression of the
CC target polynucleotide directly or indirectly promotes host cell death.
CC The cells are cultured and the insert polynucleotides are collected from
CC the cells which die. The method is useful for selecting target
CC polynucleotides, particularly polynucleotides which alter cell phenotypes
CC of induce or inhibit cell death. The method can be used to isolate toxic
CC genes such as tumour suppressors. The present sequence was used to
CC illustrate the method of the the present invention.
XX
XX
SQ Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;
XX
XX Query Match 92.6%; Score 137; DB 22; Length 149;
XX Best Local Similarity 99.3%; Pred. No. 1.6e-37;
XX Matches 148; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX 1 GGGCAAAATTTGAAAACTGATCTATTATTCGACGCGCGCCGATG-GTGGATCCCC 59
DB 1 GGGCAAAATTTGAAAACTGATCTATTATTCGACGCGCGCCGATGAGTGGATCCCC 60
XX
XX 60 GGGCTGAGGAATTCGATTCAGCTTATGATACCGCTCGAGGGGGGCGCTAAC 119
DB 61 GGGCTGAGGAATTCGATTCAGCTTATGATACCGCTCGAGGGGGGCGCTAAC 120
XX
XX 120 TAACTAATTTTGTGTTGTGGCGCGCC 148
DB 121 TAACTAATTTTGTGTTGTGGCGCGCC 149
XX
XX
RESULT 6
AD31780
ID AD31780 standard; DNA; 149 BP.
XX
XX AAD31780;
XX
XX 18-JUN-2002 (first entry)
XX
XX Modified p7.5/tk vector, p7.5/ATG2/tk.
XX
XX Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
KW vaccine; immune response; cytostatic; p7.5/tk vector; thymidine kinase;
KW p7.5/ATG2/tk vector; ds.
XX
XX Vaccinia virus.
OS

```

```

OS Synthetic.
XX
XX Key Location/Qualifiers
XX misc_signal 46..48
XX /*tag= a
XX /note= "translation start codon"
XX 117..119
XX /*tag= b
XX /note= "translation stop codon"
XX 121..123
XX /*tag= c
XX /note= "translation stop codon"
XX 125..127
XX /*tag= d
XX /note= "translation stop codon"
XX 133..139
XX /*tag= e
XX /note= "transcription stop signal"
XX
XX US2002018785-A1.
XX
XX 14-FEB-2002.
XX
XX 02-APR-2001; 2001US-0822250.
XX
XX 22-SEP-1997; 97US-0935377.
XX
XX (UVRP ) UNIV ROCHESTER.
XX
XX Zauderer M;
XX
XX WPI; 2002-239252/29.
XX
XX Representative difference Analysis method for identification of
PT antigens recognized by cytotoxic T cells and specific for human tumors,
PT comprises improved selection of genes encoding target antigens -
XX
XX Example 1; Fig 2; 54pp; English.
XX
XX The present invention relates to novel methods for the identification
CC of antigens recognised by cytotoxic T cells (CTLs) and specific for
CC human tumors, cancers and infected cells. The method involves screening
CC the products of an expression library generated from DNA/RNA of a cell
CC expressing a target epitope with cytotoxic T cells generated against
CC the cell to identify DNA clones expressing target epitope or providing
CC cytotoxic T cells specific for a gene product differentially expressed
CC by a cell and measuring the cross-reactivity of the cytotoxic T cells
CC for cells expressing a target epitope in which the target epitope is
CC identified as a gene product inducing cytotoxic T cells. The method is
CC useful for identifying a target epitope or antigen specific for a tumour
CC cell. The target epitope is also useful for identifying target antigens
CC in other target cells against which it is desirable to induce cell-
CC mediated immunity. The antigen identified by the method is useful
CC in immunogenic compositions and vaccine preparations to induce the
CC regression of tumours, cancers and infections in mammals. The method
CC also relates to vaccinia viral vectors which are useful for treating
CC tumour-bearing mammals, including humans to generate immune response
CC against the tumour cells. They are also useful for immunising or
CC vaccinating tumour-free subjects to prevent tumour formation. The
CC present sequence is modified p7.5/tk (thymidine kinase) vector,
CC p7.5/ATG2/tk. This vector comprises a vaccinia virus 7.5K promoter and
CC a modified tk DNA fragment. This vector is used in the exemplification
CC of the invention.
XX
XX
SQ Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;
XX
XX Query Match 92.6%; Score 137; DB 24; Length 149;
XX Best Local Similarity 99.3%; Pred. No. 1.6e-37;
XX Matches 148; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
XX 1 GGGCAAAATTTGAAAACTGATCTATTATTCGACGCGCGCCGATG-GTGGATCCCC 59
DB 1 GGGCAAAATTTGAAAACTGATCTATTATTCGACGCGCGCCGATGAGTGGATCCCC 60
XX

```



QY 60 GGGCTGAGGAATTCGATATCATCACTTATCGATACCGTCGACGCGGGGGCCCTAAC 119  
| | | | |  
Db 61 GGGCTGAGGAATTCGATATCATCACTTATCGATACCGTCGACGCGGGGGCCCTAAC 120  
| | | | |  
QY 120 TAACTAATTTTGTGTTGTGGCCCGGCC 148  
| | | | |  
Db 121 TAACTAATTTTGTGTTGTGGCCCGGCC 149  
| | | | |  
RESULT 7  
AAA15238  
ID AAA15238 standard; DNA; 150 BP.  
XX  
AC AAA15238;  
XX  
DT 04-SEP-2000 (first entry)  
XX  
DE Nucleotide sequence of a fragment of the plasmid p7.5/ATG3/tk.  
XX  
KM Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;  
XX vaccine; tumour regression; cancer; infection; ss.  
OS Synthetic.  
XX  
PN WO200028016-A1.  
XX  
PD 18-MAY-2000.  
XX  
PF 10-NOV-1998; 98WO-US24029.  
XX  
PR 10-NOV-1998; 98WO-US24029.  
XX  
PA (UYRP ) UNIV ROCHESTER.  
XX  
PI Zauderer M;  
XX  
DR WPI; 2000-376533/32.  
XX  
PT Novel method of identifying target epitopes or antigens specific for  
PT human tumors, cancers and infected cells involving screening expression  
PT library products of a cell expressing the target epitope  
XX  
PS Disclosure; Fig 2; 132pp; English.  
XX  
CC The present sequence represents a fragment of a vaccinia transfer  
CC plasmid, which is used in the course of the invention. The  
CC specification describes a method for identifying a target epitope.  
CC The method comprises screening the products of an expression library  
CC from a cell expressing the target epitope with cytotoxic T cells  
CC generated against the cell to identify DNA clones expressing the target  
CC epitope. The method may also comprise providing a cytotoxic T cell  
CC specific for a gene product differentially expressed by a cell and  
CC measuring the cross-reactivity of the cytotoxic T cell. The methods are  
CC useful for identifying tumour specific target epitopes and antigens which  
CC are useful in immunogenic compositions or vaccines to induce the  
CC regression of tumors, cancers or infections in mammals. The genes  
CC expressed in a panel of tumour cells that are derived from single  
CC immortalised, non-tumorigenic cell line are used to generate HLA  
CC restricted cytotoxic T cells which are evaluated for activity against  
CC tumour cells. The method is useful to identify potential antigens  
CC expressed not only by the pathogen but also by the host cells whose gene  
CC expression is altered as a result of infection. The differential gene  
CC expression strategies can be applied to identify immunogenic molecules  
CC of cells infected with virus, fungus or mycobacterium.  
XX  
SQ Sequence 150 BP; 36 A; 38 C; 39 G; 37 T; 0 other;  
Query Match 91.9%; Score 136; DB 21; Length 150;  
Best Local Similarity 98.7%; Pred. No. 3.5e-37;  
Matches 148; Conservative 0; Mismatches 0; Indels 2; Gaps 1;  
QY 1 GGCCAAAATGAAAACTAGATCTATTATTGCAAGCGGCCGCGCATG--GTGATCCCC 58

Db | | | | |  
1 GGCCAAAATGAAAACTAGATCTATTATTGCAAGCGGCCGCGCATGAGTGATCCCC 60  
| | | | |  
QY 59 CGGCGTCGAGGAATTCGATATCATCACTTATCGATACCGTCGACGCGGGGGCCCTAA 118  
| | | | |  
Db 61 CGGCGTCGAGGAATTCGATATCATCACTTATCGATACCGTCGACGCGGGGGCCCTAA 120  
| | | | |  
QY 119 CTAATAATTTTGTGTTGTGGCCCGGCC 148  
| | | | |  
Db 121 CTAATAATTTTGTGTTGTGGCCCGGCC 150  
| | | | |  
RESULT 8  
ABA01479  
ID ABA01479 standard; DNA; 150 BP.  
XX  
AC ABA01479;  
XX  
DT 04-FEB-2002 (first entry)  
XX  
DE Partial p7.5/ATG3/tk sequence.  
XX  
KM Cell death; toxic gene; tumour suppressor; ds.  
XX  
KN  
XX  
OS Synthetic.  
XX  
PN WO200172995-A2.  
XX  
PD 04-OCT-2001.  
XX  
PF 28-MAR-2001; 2001WO-US09953.  
XX  
PR 28-MAR-2000; 2000US-0192586.  
PR 10-MAY-2000; 2000US-0203343.  
PR 23-JAN-2001; 2001US-0263226.  
PR 27-FEB-2001; 2001US-0271426.  
XX  
PA (UYRP ) UNIV ROCHESTER.  
XX  
PI Zauderer M, Smith ES;  
XX  
DR WPI; 2001-570897/64.  
XX  
PT Selecting target polynucleotides, particularly toxic genes, involves  
PT introducing a library of insert polynucleotides into a host cell  
PT population, where the target polynucleotide promotes cell death  
XX  
PS Disclosure; Fig 8; 359pp; English.  
XX  
CC The present invention relates to a method for selecting a target  
CC polynucleotide. The method comprises introducing into a host cell  
CC population a library of insert polynucleotides, where expression of the  
CC target polynucleotide directly or indirectly promotes host cell death.  
CC The cells are cultured and the insert polynucleotides are collected from  
CC the cells which die. The method is useful for selecting target  
CC polynucleotides, particularly polynucleotides which alter cell phenotypes  
CC of induce or inhibit cell death. The method can be used to isolate toxic  
CC genes such as tumour suppressors. The present sequence was used to  
CC illustrate the method of the present invention.  
XX  
SQ Sequence 150 BP; 36 A; 38 C; 39 G; 37 T; 0 other;  
Query Match 91.9%; Score 136; DB 22; Length 150;  
Best Local Similarity 98.7%; Pred. No. 3.5e-37;  
Matches 148; Conservative 0; Mismatches 0; Indels 2; Gaps 1;  
QY 1 GGCCAAAATGAAAACTAGATCTATTATTGCAAGCGGCCGCGCATG--GTGATCCCC 58  
| | | | |  
Db 1 GGCCAAAATGAAAACTAGATCTATTATTGCAAGCGGCCGCGCATGAGTGATCCCC 60  
| | | | |  
QY 59 CGGCGTCGAGGAATTCGATATCATCACTTATCGATACCGTCGACGCGGGGGCCCTAA 118  
| | | | |  
Db 61 CGGCGTCGAGGAATTCGATATCATCACTTATCGATACCGTCGACGCGGGGGCCCTAA 120  
| | | | |

Oy	119	CTACTAATTTGTTTTGGGCCCGCCGC	148
Db	121	CTAACTAATTTGTTTTGCGGCCCGCCGC	150
 RESULT 9			
ID	AAD31781		
XX	AAD31781 standard; DNA; 150 BP.		
AC			
XX	AAD31781;		
DT	18-JUN-2002 (first entry)		
XX	Modified p7.5/tk vector, p7.5/ATG3/tk.		
DE			
XX			
KW	Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;		
RN	vaccine; immune response; cyostatic; p7.5/tk vector; thymidine kinase;		
KM	p7.5/ATG3/tk vector; ds.		
XX			
OS	Vaccinia virus.		
SX	Synthetic.		
FH			
FT	Key	Location/Qualifiers	
FT	misc_signal	46..48	/tag= a
FT		/note= "translation start codon"	
FT	misc_signal	118..120	/tag= b
FT		/note= "translation stop codon"	
FT	misc_signal	122..124	/tag= c
FT		/note= "translation stop codon"	
FT	misc_signal	126..128	/tag= d
FT		/note= "translation stop codon"	
FT	misc_signal	134..140	/tag= e
FT		/note= "transcription stop signal"	
PN			
XX	US2002018785-A1.		
XX			
PD	14-FEB-2002.		
XX			
PF	02-APR-2001; 2001US-0822250.		
XX			
PR	22-SEP-1997; 97US-0935377.		
XX			
PA	(UYRP ) UNIV ROCHESTER.		
PI			
XX	Zauderer M;		
DR	WPI; 2002-239252/29.		
XX			
PT	Representational Difference Analysis method for identification of		
PT	antigens recognized by cytotoxic T cells and specific for human tumors,		
PT	comprises improved selection of genes encoding target antigens -		
XX			
PS	Example 1; Fig 2; 54pp; English.		
XX			
CC	The present invention relates to novel methods for the identification		
CC	of antigens recognised by cytotoxic T cells (CTLs) and specific for		
CC	human tumours, cancers and infected cells. The method involves screening		
CC	the products of an expression library generated from DNA/RNA of a cell		
CC	expressing a target epitope with cytotoxic T cells generated against		
CC	the cell to identify DNA clones expressing target epitope or providing		
CC	cytotoxic T cells specific for a gene product differentially expressed		
CC	by a cell and measuring the cross-reactivity of the cytotoxic T cells		
CC	for cells expressing a target epitope in which the target epitope is		
CC	identified as a gene product inducing cytotoxic T cells. The method is		
CC	useful for identifying a target epitope or antigen specific for a tumour		
CC	cell. The target epitope is also useful for identifying target antigens		
CC	in other target cells against which it is desirable to induce cell-		

CC	mediated immunity. The antigen identified by the method is useful
CC	in immunogenic compositions and vaccine preparations to induce the
CC	regression of tumours, cancers and infections in mammals. The invention
CC	also relates to vaccinia viral vectors which are useful for treating
CC	tumour-bearing mammals, including humans to generate immune response
CC	against the tumour cells. They are also useful for immunising or
CC	vaccinating tumour-free subjects to prevent tumour formation. The
CC	present sequence is modified p7.5/tk (thymidine kinase) vector,
CC	p7.5/ΔG3/tk. This vector comprises a vaccinia virus 7.5K promoter and
CC	a modified tk DNA fragment. This vector is used in the exemplification
CC	of the invention.
XX	
SQ	Sequence 150 BP; 36 A; 38 C; 39 G; 37 T; 0 other;
XX	
Query Match	91.9%; Score 136; DB 24; Length 150;
Best Local Similarity	98.7%; Pred. No. 3.5e-37;
Matches 148:	Conservative 0; Mismatches 0; Indels 2; Gaps
Oy	1 GGCCTAAATTTGAAAACTAGATCTATTATTATTTGACACGGCGCGCCGATG-6TGATATCCC 58
Db	1 GGCCTAAATTTGAAAACTAGATCTATTATTATTTGACACGGCGCGCCGATGATCCCC 60
Oy	59 CGGGCTGCAGGAATTCGATATTCAGCTTATGATCCGTGCACCTCGAGGGGGGCTTAA 118
Db	61 CGGGCTGCAGGAATTCGATATTCAGCTTATGATCCGTGCACCTCGAGGGGGGCTTAA 120
Oy	119 CTACTAATTTTGTTTTGTGTGGGCCCGGCC 148
Db	121 CTACTAATTTTGTTTTGTGTGGGCCCGGCC 150
XX	
RESULT 10	
AAAI5235	
ID	AAAI5235 standard; DNA; 145 BP.
XX	
AC	AAAI5235;
XX	
DT	04-SEP-2000 (first entry)
XX	
DE	Nucleotide sequence of a fragment of the plasmid p7.5/ΔTG0/tk.
XX	
KM	Vaccinia transfer plasmid; epitope: tumour specific epitope; antigen;
XX	vaccine; tumour regression; cancer; infection; ss.
XX	
OS	Synthetic.
XX	
PN	WO200028016-A1.
XX	
PD	18-MAY-2000.
XX	
PF	10-NOV-1998; 98WO-US24029.
XX	
PR	10-NOV-1998; 98WO-US24029.
XX	
PA	(UYP) UNIV ROCHESTER.
XX	
PI	Zauderer M;
XX	
DR	WPI: 2000-376533/32.
XX	
PT	Novel method of identifying target epitopes of antigens specific for
PT	human tumors, cancers and infected cells involving screening expression
XX	library products of a cell expressing the target epitope -
XX	
PS	Disclosure; Fig 2; 132pp; English.
XX	
CC	The present sequence represents a fragment of a vaccinia transfer
CC	plasmid, which is used in the course of the invention. The
CC	specification describes a method for identifying a target epitope.
CC	The method comprises screening the products of an expression library
CC	from a cell expressing the target epitope with cytotoxic T cells
CC	generated against the cell to identify DNA clones expressing the target
CC	epitope. The method may also comprise providing a cytotoxic T cell

CC specific for a gene product differentially expressed by a cell and  
CC measuring the cross-reactivity of the cytotoxic T cell. The methods are  
CC useful for identifying tumour specific target epitopes and antigens which  
CC are useful in immunogenic compositions or vaccines to induce the  
CC regression of tumours, cancers or infections in mammals. The genes  
CC expressed in a panel of tumour cells that are derived from single  
CC immortalised, non-tumourigenic cell line are used to generate HLA  
CC restricted cytotoxic T cells which are evaluated for activity against  
CC tumour cells. The method is useful to identify potential antigens  
CC expressed not only by the pathogen but also by the host cells whose gene  
CC expression is altered as a result of infection. The differential gene  
CC expression strategies can be applied to identify immunogenic molecules  
CC of cells infected with virus, fungus or mycobacterium.

SO Sequence 145 BP; 34 A; 37 C; 38 G; 36 T; 0 other;

Query Match 89.2%; Score 132; DB 21; Length 145;  
Best Local Similarity 98.0%; Pred. No. 8.4e-36;  
Matches 145; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 GGCAGAAATGAAACTAGATCTATTATTGACGCGCGCCCATGTGATCCCG 60  
DB 1 GGCAGAAATGAAACTAGATCTATTATTGACGCGCGCCCATGTGATCCCG 57  
QY 61 GCGTCAGAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGCCTAACT 120  
DB 58 GCGTCAGAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGCCTAACT 117  
QY 121 AACTAATTTGTTTTTGTGGGCGCGCC 148  
DB 118 AACTAATTTGTTTTTGTGGGCGCGCC 145

RESULT 11

ABA01476  
ID ABA01476 standard; DNA; 145 BP.

XX ABA01476;

XX 04-FEB-2002 (first entry)

XX Partial p7.5/ATG0/tk sequence.

XX Cell death; toxic gene; tumour suppressor; ds.

XX Synthetic.

XX WO200172995-A2.

XX 04-OCT-2001.

XX 28-MAR-2001; 2001WO-US09953.

XX 28-MAR-2000; 2000US-0192586.

XX 10-MAY-2000; 2000US-0203343.

XX 23-JAN-2001; 2001US-0263226.

XX 27-FEB-2001; 2001US-0271426.

XX (UVRP ) UNIV ROCHESTER.

XX Zauderer M, Smith ES;

XX WPI; 2001-570897/64.

XX Selecting target polynucleotides, particularly toxic genes, involves  
XX introducing a library of insert polynucleotides into a host cell  
XX population, where the target polynucleotide promotes cell death -  
XX Disclosure; Fig 8; 359pp; English.

XX The present invention relates to a method for selecting a target  
XX polynucleotide. The method comprises introducing into a host cell  
XX population a library of insert polynucleotides, where expression of the

CC target polynucleotide directly or indirectly promotes host cell death.  
CC The cells are cultured and the insert polynucleotides are collected from  
CC the cells which die. The method is useful for selecting target  
CC polynucleotides, particularly polynucleotides which alter cell phenotypes  
CC of induce or inhibit cell death. The method can be used to isolate toxic  
CC genes such as tumour suppressors. The present sequence was used to  
CC illustrate the method of the present invention.

SO Sequence 145 BP; 34 A; 37 C; 38 G; 36 T; 0 other;

Query Match 89.2%; Score 132; DB 22; Length 145;  
Best Local Similarity 98.0%; Pred. No. 8.4e-36;  
Matches 145; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 GGCAGAAATGAAACTAGATCTATTATTGACGCGCGCCCATGTGATCCCG 60  
DB 1 GGCAGAAATGAAACTAGATCTATTATTGACGCGCGCCCATGTGATCCCG 57  
QY 61 GCGTCAGAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGCCTAACT 120  
DB 58 GCGTCAGAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTGAGGGGGCCTAACT 117  
QY 121 AACTAATTTGTTTTTGTGGGCGCGCC 148  
DB 118 AACTAATTTGTTTTTGTGGGCGCGCC 145

RESULT 12

AAD31778  
ID AAD31778 standard; DNA; 145 BP.

XX AAD31778;

XX 18-JUN-2002 (first entry)

XX Modified p7.5/tk vector, p7.5/ATG0/tk.

XX Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;

XX KW vaccine; immune response; cytostatic; p7.5/tk vector; thymidine kinase;

XX p7.5/ATG0/tk vector; ds.

XX Vaccinia virus.

XX Synthetic.

XX Key

XX misc\_signal

XX misc\_signal

XX misc\_signal

XX misc\_signal

XX misc\_signal

XX misc\_signal

XX misc\_signal

XX misc\_signal

XX misc\_signal

XX misc\_signal

XX misc\_signal

XX misc\_signal

XX misc\_signal

XX misc\_signal

XX misc\_signal



PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAY-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.  
XX  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
PI Schlegel R, Endege WO, Monahan JE;  
XX WPI; 2001-662795/76.  
XX  
XX Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer -  
XX  
PS Claim 1; Page 8499; 11750pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
XX  
SQ Sequence 658 BP; 176 A; 151 C; 164 G; 167 T; 0 other;  
XX  
Query Match 51.9%; Score 76.8; DB 23; Length 658;  
Best Local Similarity 75.0%; Pred. No. 1.6e-16;  
Matches 96; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
XX  
QY 6 AAATGTGAAAACCTAGATCTATTATTGACGCGCGCCCATGTGTGATCCCGGGGCTG 65  
DB 484 AATATTAGTTCCAGATCTGTACCTCGCGCTCTAGAACTAGTGAATCCCGGGGCTG 543  
QY 66 CAGGAATTCGATATCAAGCTTATCGATACCGTGAAGGGGGGGGCTACTACTA 125  
DB 544 CAGGAATTCGATATCAAGCTTATCGATACCGTGAAGGGGGGGGCTACTACTA 603  
QY 126 ATTTTGT 133  
DB 604 CTTTGT 611  
XX  
RESULT 15  
ABVA1330  
ID ABVA1330 standard; cDNA; 671 BP.  
XX  
AC ABVA1330;  
XX  
DE 16-SEP-2002 (first entry)  
XX  
DE Human prostate expression marker cDNA 41321.  
XX  
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
XX pharmacogenomic marker; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200160860-A2.  
XX  
PD 23-AUG-2001.  
XX  
PF 20-FEB-2001; 2001WO-US05171.

XX  
XX 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAY-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.  
XX  
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
PI Schlegel R, Endege WO, Monahan JE;  
XX WPI; 2001-662795/76.  
XX  
XX Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer -  
XX  
PS Claim 1; Page 8309-8310; 11750pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
XX  
SQ Sequence 671 BP; 181 A; 153 C; 167 G; 170 T; 0 other;  
XX  
Query Match 51.9%; Score 76.8; DB 23; Length 671;  
Best Local Similarity 75.0%; Pred. No. 1.6e-16;  
Matches 96; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
XX  
QY 6 AAATGTGAAAACCTAGATCTATTATTGACGCGCGCCCATGTGTGATCCCGGGGCTG 65  
DB 498 AATATTAGTTCCAGATCTGTACCTCGCGCTCTAGAACTAGTGAATCCCGGGGCTG 557  
QY 66 CAGGAATTCGATATCAAGCTTATCGATACCGTGAAGGGGGGGGCTACTACTA 125  
DB 558 CAGGAATTCGATATCAAGCTTATCGATACCGTGAAGGGGGGGGCTACTACTA 617  
QY 126 ATTTTGT 133  
DB 618 CTTTGT 625  
XX

Search completed: November 10, 2002, 05:58:28  
Job time : 175.627 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:58:40 ; Search time 36.8336 Seconds  
(without alignments)  
1425.554 Million cell updates/sec

Title: US-08-935-377-7  
 Perfect score: 148  
 Sequence: 1 GGCCAAAATGAAACTA.....TTGTTTTCGTGGCCCGGCC 148

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 320260 seqs, 177392727 residues

Total number of hits satisfying chosen parameters: 640520

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 08

Listing first 45 summaries

Database : Published\_Applications\_NA:

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1: /cgn2_6/p/odata1/1/pubnba/US07_PUBCOMB.seq.*
2: /cgn2_6/p/odata1/1/pubnba/PC91_NEW_PUB.seq.*
3: /cgn2_6/p/odata1/1/pubnba/US06_NEW_PUB.seq.*
4: /cgn2_6/p/odata1/1/pubnba/US06_PUBCOMB.seq.*
5: /cgn2_6/p/odata1/1/pubnba/US07_NEW_PUB.seq.*
6: /cgn2_6/p/odata1/1/pubnba/PC95_PUBCOMB.seq.*
7: /cgn2_6/p/odata1/1/pubnba/US08_NEW_PUB.seq.*
8: /cgn2_6/p/odata1/1/pubnba/US08_PUBCOMB.seq.*
9: /cgn2_6/p/odata1/1/pubnba/US09_NEW_PUB.seq.*
10: /cgn2_6/p/odata1/1/pubnba/US09_PUBCOMB.seq.*
11: /cgn2_6/p/odata1/1/pubnba/US10_NEW_PUB.seq.*
12: /cgn2_6/p/odata1/1/pubnba/US10_PUBCOMB.seq.*
13: /cgn2_6/p/odata1/1/pubnba/US60_NEW_PUB.seq.*
14: /cgn2_6/p/odata1/1/pubnba/US60_PUBCOMB.seq.*

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query		Length	DB	ID	Description
	Score	Match				
1	148	100.0	148	10	US-09-822-250-7	Sequence 7, Appl1
2	148	100.0	148	10	US-09-987-456-3	Sequence 8, Appl1
3	137	92.6	149	10	US-09-882-250-8	Sequence 9, Appl1
4	137	92.6	149	10	US-09-987-456-4	Sequence 4, Appl1
5	136	91.9	150	10	US-09-822-250-9	Sequence 5, Appl1
6	136	91.9	150	10	US-09-987-456-5	Sequence 6, Appl1
7	132	89.2	145	10	US-09-822-250-6	Sequence 5, Appl1
8	132	89.2	145	10	US-09-987-456-2	Sequence 2, Appl1
9	70.6	47.7	858	10	US-09-735-705-01	Sequence 91, Appl1
10	70.6	47.7	858	10	US-09-850-716A-91	Sequence 91, Appl1
11	70.6	47.7	858	10	US-09-850-716A-91	Sequence 91, Appl1
12	69.8	47.2	574	10	US-09-834-575-541	Sequence 541, Appl1
13	69.8	47.2	574	10	US-09-834-575-541	Sequence 541, Appl1
14	67.4	45.5	118	10	US-09-784-130-9	Sequence 9, Appl1
15	67.4	45.5	457	10	US-09-735-705-306	Sequence 306, Appl1
16	67.4	45.5	457	10	US-09-850-716A-306	Sequence 306, Appl1
17	67.4	45.5	457	10	US-09-897-778-306	Sequence 306, Appl1
18	67.4	45.5	752	10	US-09-956-004-108	Sequence 108, Appl1
19	67.2	45.4	545	10	US-09-810-936-10	Sequence 10, Appl1

C 20	67.2	45.4	545	10	US-09-429-755-10	Sequence 10, Appl
C 21	67.2	44.7	661	10	US-09-912-447-16	Sequence 16, Appl
C 22	62	41.9	105	10	US-09-974-300-7717	Sequence 7717, Ap
C 23	60.4	40.8	62	10	US-09-557-423-1	Sequence 1, Appl1
C 24	55.2	37.3	624	10	US-09-834-975-469	Sequence 469, Appl
C 25	54	36.5	1094	10	US-09-932-418-3	Sequence 3, Appl1
C 26	52.2	35.3	4633	10	US-09-880-107-3822	Sequence 3822, App
C 27	50.4	34.1	586	10	US-09-924-0356-701	Sequence 701, App
C 28	49.8	33.6	1981	10	US-09-908-322-26	Sequence 26, Appl1
C 29	49.8	33.6	6244	10	US-09-281-674-8	Sequence 8, Appl1
C 30	49.6	33.5	332	10	US-09-892-227-8	Sequence 14, Appl
C 31	49.4	33.4	343	10	US-09-823-114-14	Sequence 839, Appl
C 32	49.4	33.4	53	10	US-09-924-0355-839	Sequence 23, Appl
C 33	49	33.1	53	10	US-09-822-250-23	Sequence 5, Appl1
C 34	49	33.1	57	10	US-09-822-250-5	Sequence 1, Appl1
C 35	49	33.1	57	10	US-09-987-456-1	Sequence 140, App
C 36	49	33.1	69	10	US-09-822-250-1	Sequence 240, Appl
C 37	49	33.1	69	10	US-09-987-456-140	Sequence 30, Appl
C 38	49	33.1	1329	10	US-09-925-959-240	Sequence 49, Appl1
C 39	49	33.1	2790	10	US-09-739-554-30	Sequence 4, Appl1
C 40	49	33.1	2790	10	US-09-904-015-30	Sequence 19, Appl
C 41	48.4	32.7	100	10	US-09-380-1288-19	Sequence 4, Appl1
C 42	48	32.4	57	10	US-09-955-449-4	Sequence 4, Appl1
C 43	48	32.4	57	10	US-09-973-013-4	Sequence 4, Appl1
C 44	47.8	32.3	362	10	US-09-925-0100-903	Sequence 903, App
C 45	47.4	32.0	341	10	US-09-735-705-302	Sequence 302, App

## ALIGNMENTS

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RESULT 1
US-09-822-250-7
Sequence 7, Application US/09822250
Patent No. US20020018785A1
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
FILE REFERENCE: 1821.0010001
CURRENT APPLICATION NUMBER: US/09/822,250
CURRENT FILING DATE: 2001-04-02
PRIORITY APPLICATION NUMBER: US 08/935,377
PRIORITY FILING DATE: 1997-09-22
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
LENGTH: 148
TYPE: DNA
ORGANISM: synthetic construct
US-09-822-250-7

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Query Match	100.0%;	Score 148;	DB 10;	Length 148;
Best Local Similarity	100.0%;	Pred. No. 3.8e-47;		
Matches 148;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	GGCAAAAATTTAAAAATCATATCTATTTTTCACGGGGCCGCATGGTGTGATCCCCG	60
Db	1	GGCAAAAATTTGAAAACTCATCTATTATTATTCACGGGGCCGCCCATGTGGATCCCCG	60
Qy	61	GGCTGAGGAANTGATATCAAGCTTATCGATACGCTGCAGGGGGGGCCTAACT	120
Db	61	GGCTGAGGAANTGATATCAAGCTTATCGATACGCTGCAGGGGGGGCCTAACT	120
Qy	121	AACTAATTTTGTGTTTGTGGGCCCGGCC	148
Db	121	AACTAATTTTGTGTTTGTGGGCCCGGCC	148

RESULT 2  
US-09-987-456-3  
Sequence 3, Application US/09987456  
Patent No. US20020123057A1  
GENERAL INFORMATION:

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; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; APPLICANT: Ernest S. Smith
; TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
; TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
; FILE REFERENCE: 1821.0070004
; CURRENT APPLICATION NUMBER: US/09/987,456
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/271,424
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/262,067
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/298,087
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/249,268
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 148
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p 7.5/ATG1/tk promoter
US-09-987-456-3

Query Match
Best Local Similarity 100.0%; Score 148; DB 10; Length 148;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GGGCAAAATTTGAAAACATGATCTATTATTATTCACGCGGCCCATGTGATCCCGG 60
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DB 1 GGGCAAAATTTGAAAACATGATCTATTATTATTCACGCGGCCCATGTGATCCCGG 60
    |||||||
QY 61 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTTCGACCTCGAGGGGGCCTTA 120
    |||||||
DB 61 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTTCGACCTCGAGGGGGCCTTA 120
    |||||||
QY 121 AACTAATTTGTTTGTGGGGCCGCC 148
    |||||||
DB 121 AACTAATTTGTTTGTGGGGCCGCC 148
    |||||||
```

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RESULT 3
US-09-822-250-8
; Sequence 8, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 149
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-822-250-8
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Query Match
Best Local Similarity 92.6%; Score 137; DB 10; Length 149;
Matches 148; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGGCAAAATTTGAAAACATGATCTATTATTATTCACGCGGCCCATGTGATCCCGG 59
    4|||||
DB 1 GGGCAAAATTTGAAAACATGATCTATTATTATTCACGCGGCCCATGTGATCCCGG 60
    |||||||
QY 60 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTTCGACCTCGAGGGGGCCTTA 119
    |||||||
```

```

DB 61 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTTCGACCTCGAGGGGGCCTTA 120
QY 120 TAATAATTTGTTTGTGGGGCCGCC 148
    |||||||
DB 121 TAATAATTTGTTTGTGGGGCCGCC 149
    |||||||
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RESULT 4
US-09-987-456-4
; Sequence 4, Application US/09987456
; Patent No. US20020123057A1
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; APPLICANT: Ernest S. Smith
; TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
; TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
; FILE REFERENCE: 1821.0070004
; CURRENT APPLICATION NUMBER: US/09/987,456
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/271,424
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/262,067
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/298,087
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/249,268
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 149
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p7.5/ATG2/tk vector
US-09-987-456-4
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Query Match
Best Local Similarity 92.6%; Score 137; DB 10; Length 149;
Matches 148; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGGCAAAATTTGAAAACATGATCTATTATTATTCACGCGGCCCATGTGATCCCGG 59
    |||||||
DB 1 GGGCAAAATTTGAAAACATGATCTATTATTATTCACGCGGCCCATGTGATCCCGG 60
    |||||||
QY 60 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTTCGACCTCGAGGGGGCCTTA 119
    |||||||
DB 61 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTTCGACCTCGAGGGGGCCTTA 120
    |||||||
QY 120 TAATAATTTGTTTGTGGGGCCGCC 148
    |||||||
DB 121 TAATAATTTGTTTGTGGGGCCGCC 149
    |||||||
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RESULT 5
US-09-822-250-9
; Sequence 9, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 150
; TYPE: DNA
; ORGANISM: synthetic construct
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	Query Match	89.2%	Score 132	DB 10	Length 145
	Best Local Similarity	98.0%	Prod. No. 4,9e-41		
	Matches 145	Conservative 0	Mismatches 0	Indels 3	Gaps 1
20Y	1	GGCCAAAATGAAAACACTACATCTATTATTTGACGCGCGCCCATGTTGATCCCGG	60		
20Y	1	GGCCAAAATGAAAACACTACATCTATTATTTGACGCGCGCCCGC--GTGATCCCGG	57		
61	GGCTGCGAGGATTGATATCAAGCTTATGCAATCCGTGACCTCGAGGGGGGCGCTTA	120			
58	GGCTGCGAGGATTGATATCAAGCTTATGCAATCCGTGACCTCGAGGGGGGCGCTTA	117			

Qy	121	AACTAATTTGTTTGTGGCCCGGCC	148
Db	118	AACTAATTTGTTTGTGGCCCGGCC	145

RESULT 9  
US-09-735-705-91

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Sequence 91, Application US/09735705
Patent No. US20020052329A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Jiqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 91
LENGTH: 858
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(858)
OTHER INFORMATION: n = A,T,C or G
US-09-735-705-91

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Query Match	47.7%	Score 70.6	DB 10	Length 858
Best Similarity	84.9%	Pred. No. 3.2e-17		
Best Local Match 79	Conservative	0	Mismatches 14	Indels 0
			Gaps	0

Dy      23 TCTATTATTCGACGGCGGCCCATGTGCATCCCCGGGTGCAGAA TTCGATA TC AA 82  
||| ||| | | | | | | | | | | | | | |  
Db    331 TCACGAATTC CACCACACTG GACTAGTGCATCCCCGGGTGCAGAA TTCGATA TC AA 390

QY 83 GCTATCAGTACCGTCGACCTCGAGGGGGGCC 115  
 |||||  
 Db 391 GCTTATCGATCCGTCGACCTCGAGGGGGGCC 423

RESULT 10  
US-09-850-716A-91

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? Sequence 91, Application US/09850716A
? Patent No. US2002011539A1
? GENERAL INFORMATION:
? APPLICANT: Kalos, Michael D.
? APPLICANT: McNeill, Patricia D.
? APPLICANT: Retter, Marc W.
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? OF INFECTIONS AND DIAGNOSIS OF LUNG CANCER
? FILE REFERENCE: 210121.455C15
? CURRENT APPLICATION NUMBER: US/09/850,716A
? CURRENT FILING DATE: 2001-05-07
? NUMBER OF SEQ ID NOS: 440
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 91
? LENGTH: 838
? TYPE: DNA
? ORGANISM: Homo sapien
? FEATURE: >

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; NAME/KEY: misc_feature
; LOCATION: (1)...(858)
; OTHER INFORMATION: n = A,T,C or G
US-09-850-716A-91

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Query Match	47.7%;	Score 70.6;	DB 10;	Length 858;
Similarity	84.9%;	Pred. No. 3.2e-17;		
Best Local				
Matches 79; Conservative	0;	Mismatches 14;	Indels 0;	Gaps 0;

OY	23	TCATATTATTGACGGGGCCCATGGTGGATCCCCGGGCTGCAGAAATTCGATTATCAA	82
Db	331	TCACGAATTTCCACACACCTGAGACTAATGATATCCCCGGGCTGCAGAAATTCGATTCAA	390
OY	83	GCTTATCGATTACCGTCGACCTTCGAGGGGGGGCC	115
OY	391	GCTTATCGATTACCGTCGACCTTCGAGGGGGGGCC	423

RESULT 11  
US-09-897-778-91

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? Sequence 91, Application Us/05967710
? Patent No. US20020147143A1
?
? GENERAL INFORMATION:
?
? APPLICANT: Wang, Tonglong
?
? APPLICANT: Marnerakis, Margarita
?
? APPLICANT: Fanger, Gary R.
?
? APPLICANT: Vedvick, Thomas S.
?
? APPLICANT: Carter, Darick
?
? APPLICANT: Matanabe, Yoshihiro
?
? APPLICANT: Henderson, Robert A.
?
? APPLICANT: Peckham, David W.
?
? APPLICANT: Fanger, Neil
?
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
?
? TITLE OF INVENTION: AND DIAGNOSTS OF LUNG CANCER
?
? FILE REFERENCE: 210121.455616
?
? CURRENT APPLICATION NUMBER: US/09/897,778
?
? CURRENT FILING DATE: 2001-06-28
?
? NUMBER OF SEQ ID NOS: 467
?
? SOFTWARE: FastSeq for Windows Version 4.0
?
? SEQ ID NO 91
?
? LENGTH: 858
?
? TYPE: DNA
?
? ORGANISM: Homo sapiens
?
? FEATURE:
?
? NAME/KEY: misc_feature
?
? LOCATION: 570..591, 655, 664, 667, 683, 711, 759, 760, 765, 777, 787
?
? LOCATION: 792, 794, 801, 804, 809, 817, 820
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? OTHER INFORMATION: n = A,T,C or G
?
US-08-897-778-91

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Query Match	47.78;	Score 70.6;	DB 10;	Length 858;
Best Local Similarity	84.98;	Pred. No. 3.2e-17;		
Matches 79; Conservative		0; Mismatches 14;	Indels 0;	Gaps 0;

[illegible]

QY 83 GCTTATCGATACCGTCGACCTCGAGGGGGGCC 115  
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 Db 391 GCTTATCGATACCGTCGACCTCGAGGGGGGCC 423

RESULT  
US-09-81

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: Sequence 541, Application US/09834975
: Patent No. US20020110815A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Lillie, James
: APPLICANT: Brown, Jeffrey
: APPLICANT: Bolt, Andrew
: APPLICANT: Van Hufel, Christophe
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS

```

```
; TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF HUMAN CANCERS
; FILE REFERENCE: MRI-016B
; CURRENT APPLICATION NUMBER: US/09/834,975
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,538
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 1046
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 541
; LENGTH: 574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-975-541
```

```
Query Match          47.2%; Score 69.8; DB 10; Length 574;
Best Local Similarity 73.6%; Pred. No. 5.4e-17;
Matches 89; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
```

```
OY 13 AAAACGTAGCTATTATTCAGCGCGCCCATGGTGGATCCCGCGCTGAGGAAT 72
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 134 AACGTTAAATTTACACCTCGCGCTCTAGACTAGTGGATCCCGCGCGAGAAC 75
OY 73 TCGATATCAACCTTATGATACCTCGACCTCGAGGGGGGCTTAACCTATTGTT 132
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 74 TCGATATCAACCTTATGATACCTCGACCTCGAGGGGGGCGGTACCCAGCTTTGT 15
OY 133 T 133
Db 14 T 14
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```
RESULT 13
US-09-834-975-601/C
; Sequence 601, Application US/09834975
; Patient No. US20020110815A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Brown, Jeffrey
; APPLICANT: Bolt, Andrew
; APPLICANT: Van Huffel, Christophe
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-016B
; CURRENT APPLICATION NUMBER: US/09/834,975
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,538
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 1046
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 601
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-975-601
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Query Match          46.9%; Score 69.4; DB 10; Length 424;
Best Local Similarity 87.4%; Pred. No. 6.6e-17;
Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
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OY 47 TGGTGGATCCCCGGGCTGAGGAATTCGATATCAAGCTTATGATACCTGAGCTCGA 106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 106 TAGTGGATCCCCGGGCTGAGGAATTCGATATCAAGCTTATGATACCTGAGCTCGA 47
OY 107 GGGGGGCTTAACCTAATTTGTT 133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 46 GGGGGGCTTAACCTAATTTGTT 20
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```
RESULT 14
US-09-784-130-9/C
; Sequence 9, Application US/09784130
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; Patent No. US20020076808A1
; GENERAL INFORMATION:
; APPLICANT: Donahue, Brian A.
; APPLICANT: Hardy, Stephen F.
; APPLICANT: Snyder, Richard O.
; APPLICANT: Cell Genesys, Inc.
; TITLE OF INVENTION: USE OF SUPPRESSOR tRNA's TO REGULATE CYTOTOXICITY
; TITLE OF INVENTION: DURING THE PRODUCTION OF RECOMBINANT GENE PRODUCTS
; FILE REFERENCE: P132222
; CURRENT APPLICATION NUMBER: US/09/784,130
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/097,328
; PRIOR FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 118
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: polylinker
US-09-784-130-9
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```
Query Match          45.5%; Score 67.4; DB 10; Length 118;
Best Local Similarity 98.6%; Pred. No. 2e-16;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 47 TGGTGGATCCCCGGGCTGAGGAATTCGATATCAAGCTTATGATACCTGAGCTCGA 106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 93 TAGTGGATCCCCGGGCTGAGGAATTCGATATCAAGCTTATGATACCTGAGCTCGA 34
OY 107 GGGGGGCTTAACCTAATTTGTT 133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 33 GGGGGGCTTAACCTAATTTGTT 25
```

```
RESULT 15
US-09-735-705-306
; Sequence 306, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 306
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-735-705-306
```

```
Query Match          45.5%; Score 67.4; DB 10; Length 457;
Best Local Similarity 98.6%; Pred. No. 3.9e-16;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 47 TGGTGGATCCCCGGGCTGAGGAATTCGATATCAAGCTTATGATACCTGAGCTCGA 106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Db 358 TAGTGATCCCCGGGCTGCAGAAATTCATATCAAGCTTATCGATAACGTCGACCTCGA 417

OY 107 GGGGGGGCC 115  
|||||

Db 418 GGGGGGGCC 426

Search completed: November 10, 2002, 11:33:46  
Job time : 37.836 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:43:30 : Search time 37.943 Seconds  
(without alignments)  
1196.219 Million cell updates/sec

Title: US-08-935-377-7

Perfect score: 148  
Sequence: 1 GGCCAAAATGAAAACTA.....TTGTTTGTGGCCCGGCC 148

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA.\*

1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCrus.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70.6	47.7	858	4	US-09-123-912-91
2	70.6	47.7	858	4	US-09-643-597-91
3	69.4	46.9	229	4	US-09-116-482A-39
4	68.4	46.2	793	2	US-08-967-101-121
5	68.4	46.2	793	2	US-08-592-541-121
6	68.4	46.2	793	3	US-09-124-698-121
7	68.4	46.2	793	4	US-09-127-480-121
8	68.4	46.2	793	4	US-08-496-841C-121
9	68.4	46.2	793	4	US-09-124-523-121
10	68	45.9	5356	4	US-08-446-935-1
11	67.4	45.5	147	4	US-09-323-872A-26
12	67.4	45.5	457	4	US-09-643-597-306
13	67.4	45.5	752	4	US-08-976-259-108
14	67.4	45.5	2961	4	US-08-446-935-6
15	67.4	45.5	3792	2	US-08-992-334-1
16	67.4	45.5	3792	2	US-08-302-752-1
17	67.4	45.5	4016	1	US-08-410-540-3
18	67.4	45.5	5234	3	US-08-992-334-2
19	67.4	45.5	5234	3	US-08-302-752-2
20	67.4	45.5	5592	4	US-09-495-797-37
21	67.4	45.5	6722	2	US-08-992-334-3
22	67.4	45.5	6722	3	US-08-302-752-3
23	67.2	45.4	545	4	US-08-991-789A-10
24	67.2	45.4	545	4	US-09-062-451-10
25	67.2	45.4	545	4	US-09-598-326-10
26	66	44.6	11233	4	US-08-980-832-27
27	65.4	44.2	9318	2	US-08-793-610-6

28	65.2	44.1	713	4	US-08-998-416-135	Sequence 135, App
C	65	43.9	78	4	US-09-462-645C-25	Sequence 25, Appl
30	65	43.9	84	4	US-09-462-645C-26	Sequence 26, Appl
31	65	43.9	698	4	US-08-998-416-54	Sequence 54, Appl
C	32	65	3465	4	US-09-462-645C-9	Sequence 9, Appl
C	33	65	43.9	4	US-09-462-645C-11	Sequence 11, Appl
C	34	65	43.9	4	US-09-462-645C-5	Sequence 5, Appl
C	35	65	43.9	4	US-09-462-645C-7	Sequence 7, Appl
C	36	65	43.9	4	US-09-575-602-11	Sequence 11, Appl
37	62.8	42.4	685	1	US-08-465-388-56	Sequence 56, Appl
38	59.6	42.4	685	1	US-08-204-675-1	Sequence 1, Appl
39	59.6	40.3	4164	2	US-08-560-754-1	Sequence 1, Appl
40	59.6	40.3	4164	2	US-08-796-364-1	Sequence 1, Appl
41	59.6	40.3	4164	5	PCT-US95-02520-1	Sequence 54, Appl
42	58.4	39.3	5178	2	US-08-474-169-2	Sequence 2, Appl
43	58.2	39.3	3198	4	US-08-842-306B-48	Sequence 48, Appl
44	58.2	39.3	3198	4	US-08-838-973B-48	Sequence 48, Appl
45	58.2	39.3	3198	4	US-08-838-973B-48	Sequence 48, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-123-912-91
Sequence 91, Application US/09123912A
Patent No. 6312695
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REFERENCE: 210121.455c1
CURRENT APPLICATION NUMBER: US/09/123,912A
PRIOR FILING DATE: 1998-07-27
PRIORITY APPLICATION NUMBER: 09/040,802
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 91
LENGTH: 858
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (570)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (591)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (655)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (664)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (667)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (683)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (711)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (759)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (760)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (765)
OTHER INFORMATION: Where n is a, c, g or t
```

```
NAME/KEY: modified_base
LOCATION: (777)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (787)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (792)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (794)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (801)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (804)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (809)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (817)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (820)
OTHER INFORMATION: where n is a, c, g or t
US-09-123-912-91
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Query Match 47.7%; Score 70.6; DB 4; Length 858;

Best Local Similarity 84.9%; Pred. No. 1.8e-14; Matches 79; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```
QY 23 TCTATTATTCACGCCGCCCATGTGTGATCCCGGGCTGCAGATTCGATATCAA 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 331 TCAACGATTCACACACACTGACTAGTATCCCGGGCTGCAGATTCGATATCAA 390
QY 83 GCTATCGATACCGTCGACCTCGAGGGGGGCC 115
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 391 GCTATCGATACCGTCGACCTCGAGGGGGGCC 423
```

#### RESULT 2

US-09-643-597-91

Sequence 91, Application US/09643597

Patent No. 6426072

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Fan, Liqun

APPLICANT: Kaios, Michael D.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: Hosken, Nancy

APPLICANT: Fanger, Gary R.

APPLICANT: Li, Samuel X.

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.455C11

CURRENT APPLICATION NUMBER: US/09/643.597

CURRENT FILING DATE: 2000-08-21

NUMBER OF SEQ ID NOS: 369

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 91

LENGTH: 858

TYPE: DNA

ORGANISM: Homo sapien

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (1)...(858)

OTHER INFORMATION: n = A,T,C or G

US-09-643-597-91

Query Match 47.7%; Score 70.6; DB 4; Length 858;

Best Local Similarity 84.9%; Pred. No. 1.8e-14; Matches 79; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```
QY 23 TCTATTATTCACGCCGCCCATGTGTGATCCCGGGCTGCAGATTCGATATCAA 82
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 331 TCAACGATTCACACACACTGACTAGTATCCCGGGCTGCAGATTCGATATCAA 390
QY 83 GCTATCGATACCGTCGACCTCGAGGGGGGCC 115
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 391 GCTATCGATACCGTCGACCTCGAGGGGGGCC 423
```

#### RESULT 3

US-09-116-492A-39/C

Sequence 39, Application US/09116492A

Patent No. 6436409

GENERAL INFORMATION:

APPLICANT: GICOUEL, BRIGITTE

APPLICANT: BERTHET, FRANCOIS-XAVIER

APPLICANT: ANDERSEN, PETER

APPLICANT: RASMUSSEN, PETER B

TITLE OF INVENTION: POLYNUCLEOTIDE FUNCTIONALLY CODING FOR THE LHP PROTEIN FROM MY

TITLE OF INVENTION: TOBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGMENTS, A

FILE REFERENCE: 0660-0137-27X

CURRENT APPLICATION NUMBER: US/09/116.492A

CURRENT FILING DATE: 1998-07-16

PRIOR APPLICATION NUMBER: 60/252.631

PRIOR FILING DATE: 1997-07-16

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin version 3.1

SEQ ID NO 39

LENGTH: 229

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: multiple cloning site-artificial DNA

US-09-116-492A-39

Query Match 46.9%; Score 69.4; DB 4; Length 229;

Best Local Similarity 87.4%; Pred. No. 3.1e-14; Matches 76; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```
QY 47 TGGTGAATCCCGGGGCTGCAGATTCGATATCAAGCTTATCGATACCGTGCACCTCGA 106
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 142 TAGTGAATCCCGGGGCTGCAGATTCGATATCAAGCTTATCGATACCGTGCACCTCGA 83
QY 107 GGGGGGGCTTAACCTAATTTTGT 133
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 82 GGGGGGGGGCTTAACCTAATTTTGT 56
```

#### RESULT 4

US-08-967-101-121/C

Sequence 121, Application US/08967101

Patent No. 5840540

GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H

APPLICANT: ROMMERS, JOHANNA M

APPLICANT: FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

TITLE OF INVENTION: TO ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 183

CORRESPONDENCE ADDRESS:

ADDRESSEE: TESTA, HURWITZ & THIBEAULT

STREET: High Street Tower - 125 High Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/967,101  
FILING DATE: 10-NOV-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/592,541  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 793 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-967-101-121

Query Match 46.2%; Score 68.4; DB 2; Length 793;  
Best Local Similarity 87.2%; Pred. No. 9.4e-14;

Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 48 GGTGATCCCCCGGCTGCAGGAATTCGATATCAAGCTTATCGTACCGTCGACCTCGAG 107  
DB 119 GGGGATCCCCCGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 60  
QY 108 GGGGGCCTAAGTAATTAATTTGTT 133  
DB 59 GGGGGCCCGGTACCAAGCTTTGTT 34

RESULT 5  
US-08-592-541-121/c  
Sequence 121, Application US/08592541  
Patent No. 5986054  
GENERAL INFORMATION:  
APPLICANT: ST. GEORGE-HYSLOP, PETER H  
APPLICANT: ROMMENS, JOHANNA M  
APPLICANT: FRASER, PAUL E  
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TO ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 183  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
STREET: High Street Tower - 125 High Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/592,541  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:

LENGTH: 793 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-592-541-121

Query Match 46.2%; Score 68.4; DB 2; Length 793;  
Best Local Similarity 87.2%; Pred. No. 9.4e-14;  
Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 48 GGTGATCCCCCGGCTGCAGGAATTCGATATCAAGCTTATCGTACCGTCGACCTCGAG 107  
DB 119 GGGGATCCCCCGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 60  
QY 108 GGGGGCCTAAGTAATTAATTTGTT 133  
DB 59 GGGGGCCCGGTACCAAGCTTTGTT 34

RESULT 6  
US-09-124-698-121/c  
Sequence 121, Application US/09124698  
Patent No. 6117978  
GENERAL INFORMATION:  
APPLICANT: ST. GEORGE-HYSLOP, PETER H  
APPLICANT: ROMMENS, JOHANNA M  
APPLICANT: FRASER, PAUL E  
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
TO ALZHEIMER'S DISEASE  
NUMBER OF SEQUENCES: 183  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
STREET: High Street Tower - 125 High Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/124,698  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/592,541  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 793 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-124-698-121

Query Match 46.2%; Score 68.4; DB 3; Length 793;  
Best Local Similarity 87.2%; Pred. No. 9.4e-14;  
Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 48 GGTGATCCCCCGGCTGCAGGAATTCGATATCAAGCTTATCGTACCGTCGACCTCGAG 107  
DB 119 GGGGATCCCCCGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 60  
QY 108 GGGGGCCTAAGTAATTAATTTGTT 133

Db 59 GGGGGGCCGGTACCCAGCTTTGTT 34

## RESULT 7

US-09-127-480-121/c  
; Sequence 121, Application US/09127480  
; Patent No. 6194153  
; GENERAL INFORMATION:  
; APPLICANT: ST. GEORGE-HYSLOP, PETER H  
; APPLICANT: ROMMENS, JOHANNA M  
; APPLICANT: FRASER, PAUL E  
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE  
; NUMBER OF SEQUENCES: 183  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
; STREET: High Street tower - 125 High Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/127,480  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/592,541  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pitcher, Edmund R.  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 248-7000  
; TELEFAX: (617) 248-7100  
; INFORMATION FOR SEQ ID NO: 121:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 793 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-09-127-480-121

Query Match 46.2%; Score 68.4; DB 4; Length 793;  
Best Local Similarity 87.2%; Pred. No. 9.4e-14;  
Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 48 GGTGATCCCCCGGCGAGCAATTCATATCAAGCTTATCGATACCGCGACCTCGAG 107  
|| |||||  
Db 119 GCGGATCCCCCGGCGAGCAATTCATATCAAGCTTATCGATACCGCGACCTCGAG 60  
OY 108 GGGGGCCCTAAGTAATTTGTT 133  
|| |||||  
Db 59 GGGGGCCCGTACCCAGCTTTGTT 34

## RESULT 8

US-08-496-841C-121/c  
; Sequence 121, Application US/08496841C  
; Patent No. 6210919  
; GENERAL INFORMATION:  
; APPLICANT: ST. GEORGE-HYSLOP, PETER H  
; APPLICANT: ROMMENS, JOHANNA M  
; APPLICANT: FRASER, PAUL E  
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE  
; NUMBER OF SEQUENCES: 175  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Darby & Darby, PC  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/496,841C  
FILING DATE: 28-Jun-1995  
CLASSIFICATION: <Unknown>

## ATTORNEY/AGENT INFORMATION:

NAME: Paul F. Fehner, Ph.D.

## REGISTRATION NUMBER: 35,135

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 527-7700

TELEFAX: (212) 753-6237

INFORMATION FOR SEQ ID NO: 121:

SEQUENCE CHARACTERISTICS:

LENGTH: 793 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 121:

US-08-496-841C-121

Query Match 46.2%; Score 68.4; DB 4; Length 793;  
Best Local Similarity 87.2%; Pred. No. 9.4e-14;  
Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 48 GGTGATCCCCCGGCGAGCAATTCATATCAAGCTTATCGATACCGCGACCTCGAG 107  
|| |||||  
Db 119 GCGGATCCCCCGGCGAGCAATTCATATCAAGCTTATCGATACCGCGACCTCGAG 60  
OY 108 GGGGGCCCTAAGTAATTTGTT 133  
|| |||||  
Db 59 GGGGGCCCGTACCCAGCTTTGTT 34

## RESULT 9

US-09-124-523-121/c  
; Sequence 121, Application US/09124523  
; Patent No. 6395960  
; GENERAL INFORMATION:  
; APPLICANT: ST. GEORGE-HYSLOP, PETER H  
; APPLICANT: ROMMENS, JOHANNA M  
; APPLICANT: FRASER, PAUL E  
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED  
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE  
; NUMBER OF SEQUENCES: 183  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT  
; STREET: High Street Tower - 125 High Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/124,523  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/592,541



FILED DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 793 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-124-523-121

Query Match 46.2%; Score 68.4; DB 4; Length 793;  
Best Local Similarity 87.2%; Pred. No. 9.4e-14;  
Matches 75; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 48 GGGGATCCCCCGGCTGCGAGATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 107  
DB 119 GGGGATCCCCCGGCTGCGAGATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 60  
QY 108 GGGGAGCTTACTACTAATTTGTT 133  
DB 59 GGGGAGCTTACTACTAATTTGTT 34

RESULT 10  
US-08-446-935-1/C  
Sequence 1, Application US/08446935  
Patent No. 6187991  
GENERAL INFORMATION:  
APPLICANT: Soeller, Walter C.  
APPLICANT: Kreuter, David K.  
TITLE OF INVENTION: TRANSGENIC ANIMAL MODELS FOR TYPE II  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pfizer Inc.  
STREET: 235 East 42nd Street, 20th Floor  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10017-5755  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,935  
FILING DATE:

CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Sheyfa, Robert F.  
REGISTRATION NUMBER: 31,304  
REFERENCE/DOCKET NUMBER: PC8153  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)573-1189  
TELEFAX: (212)573-1939  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5356 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
US-08-446-935-1

Query Match 45.9%; Score 68; DB 4; Length 5356;

Best Local Similarity 88.1%; Pred. No. 2.2e-13;  
Matches 74; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 32 TGCACGGGCCCCCATGTGATCCCGGGCTGCGAGATTCGATATCAAGCTTATCGA 91  
DB 743 TCCACTTGGAGTGTGGGGGATCCCGGGCTGCGAGATTCGATATCAAGCTTATCGA 684  
QY 92 TACCGTCGACCTCGAGGGGGGCC 115  
DB 683 TACCGTCGACCTCGAGGGGGGCC 660

RESULT 11  
US-09-323-872A-26/C  
Sequence 26, Application US/09323872A  
Patent No. 6395359  
GENERAL INFORMATION:  
APPLICANT: Coschigano, Peter  
TITLE OF INVENTION: Compositions and Methods for Bioremediation  
FILE REFERENCE: OHU-03640  
CURRENT APPLICATION NUMBER: US/09/323,872A  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 09/072,433  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: Patent version 3.0  
SEQ ID NO 26  
LENGTH: 147  
TYPE: DNA  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(147)  
US-09-323-872A-26

Query Match 45.5%; Score 67.4; DB 4; Length 147;  
Best Local Similarity 98.6%; Pred. No. 1.3e-13;  
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 47 TGTGATCCCCCGGCTGCGAGATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106  
DB 108 TAGTGTATCCCCCGGCTGCGAGATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 49  
QY 107 GGGGGGGCC 115  
DB 48 GGGGGGGCC 40

RESULT 12  
US-09-643-597-306  
Sequence 306, Application US/09643597  
Patent No. 6426072  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C11  
CURRENT APPLICATION NUMBER: US/09/643,597  
PRIOR FILING DATE: 2000-08-21  
NUMBER OF SEQ ID NOS: 369  
SOFTWARE: FastSeq for Windows version 3.0  
SEQ ID NO 306  
LENGTH: 457

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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-643-597-306

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Query Match	45.5%;	Score 67.4;	DB 4;	Length 457;
Best Local Similarity	98.6%;	Pred. No. 1.7e-13;		
Matches 68;	Conservative	0;	Mismatches 1;	Indels

**Oy**    47 TGGTGGATCCCCCGGCTGCAGAAITCGATCAAGCTTATCGATACCGTCGACCTCGA 106  
         | |||||  
**Db**    358 TAGTGGAITCCCCCGGCTGCAGGAATTCGATCAAGCTTATCGATACCGTCGACCTCGA 417

QY	107	GGGGGGCC	115
Db	418	GGGGGGCC	426

RESULT 13  
US-08-976-259-108/c  
; Sequence 108, Application US/08976255

GENERAL INFORMATION:  
 APPLICANT: Dillon, Patrick J.  
 APPLICANT: Choi, Gil H.  
 APPLICANT: Welch, Rodney A.  
 TITLE OF INVENTION: Nucleotide Sequence of *Escherichia coli*

NUMBER OF SEQUENCES: 142  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & F  
STREET: 1100 New York Ave, N.W., Suite 600  
CITY: Washington

COUNTRY: USA  
ZIP: 20005-3934

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII TEXT  
CURRENT APPLICATION DATA:  
CURRENT DATE/TIME: 11/11/80 11:00

APPLICATION NUMBER: 05/08/310,233  
FILING DATE: Herewith  
CORRESPONDENCE: 536

CLASSIFICATION: C  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/031 626 AND US 60/061 953

ATTORNEY/AGENT INFORMATION:  
NAME: Steffe, Eric K.

REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0740002/EKS/CBM

TELECOMMUNICATION INFORMATION  
TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 108:

SEQUENCE CHARACTERISTICS:  
LENGTH: 752 base pairs

TYPE: nucleic acid  
STRANDEDNESS: double  
MONOMER: 1 base

10F00001 :  
MS-08-976-259-108

Query Match	45.5%	Score 67.4;	DB 4;	Length 752;
Best Local Similarity	98.6%;	Pred. No. 2e-13;		
Matches 68;	Conservative	0;	Mismatches 1;	Indels 0;
			Gaps	0

**QY**    47 TGGTGAATCCCCCGGCTGCAGAAATTCGATTCAAGCTTATCGAATACCGGTGACCCTCGA 106  
       | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
**Db**    74 TAGTGATCCCGCGGGCTGCAGAAATTCGATTCAAGCTTATCGAATACCGGTGACCCTCGA 15

QY	103	GGGGGGCC	11
Db	14	GGGGGGCC	6

RESULT 14  
US-08-446-935-6/c  
; Sequence 6, Application US/08446935  
; Patent No. 6187991

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```

ADDRESS: Pfizer Inc.  
STREET: 235 East 42nd Street, 20th Floor  
CITY: New York

COONIN: 0.8.8.  
ZIP: 10017-5755  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy

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ATTORNEY/AGENT INFORMATION:

NAME: SNEYDA, ROBERT F.  
REGISTRATION NUMBER: 31,304  
REFERENCE NUMBER: PC8155  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 512-2200  
TELEFAX: (212) 512-2200  
TELEX: N/A

TELEA: N/A  
; INFORMATION FOR SEQ ID NO: 6  
; SEQUENCE CHARACTERISTICS:

SEQUENCE CHANGES  
LENGTH: 2961 base pairs  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)  
; NS-08-446-935-6

Query Match 45.58; Score 67.4; DB 4; Length 2961;

Best Local Similarity 98.6%; Pred. No. 2.9e-13;  
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0

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Oy      47  TGTGGATCCCCCGGCTGCAGAAATTCATATCAAGCTTATCGAATACCGTCGACCTCGA  106
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Db      728  TAGTGGATCCCCCGGCTGCAGAAATTCATATCAAGCTTATCGAATACCGTCGACCTCGA  665

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QY	107	GGGGGGGCC	115
Db	668	GGGGGGGCC	660

RESULT 15  
US-08-992-334-1/c  
: Sequence 1, Application US/08992334

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: Patent No. 59196/8
:
: GENERAL INFORMATION:
:
: APPLICANT: Gruss, Alexandra
:
: APPLICANT: Maquin, Emmanuelle
:

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; TITLE OF INVENTION:  METHODS FOR USING A TEMPERATURE SENSITIVE
; TITLE OF INVENTION:  PLASMID
; NUMBER OF SEQUENCES:  3
; CORRESPONDENCE ADDRESS:

```

ADDRESS: Christie Parker & Hale, LLP  
STREET: 350 West Colorado Boulevard, Suite 500  
CITY: Pasadena  
STATE: California





GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:05:45 ; Search time 724.448 Seconds

(without alignments)  
5985.683 Million cell updates/sec

Title: US-08-935-377-8

Perfect score: 149

Sequence: 1 GGCCAAAATGTGAAAACCTA.....TTGTTTGTGCGCCGCCGCC 149

Scoring table: IDENTITY\_NUC

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_hlg:\*  
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8: gb\_pl:\*  
9: gb\_pr:\*  
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11: gb\_sts:\*  
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20: em\_cm:\*  
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23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
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31: em\_hlg\_inv:\*  
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36: em\_hlg\_mam:\*  
37: em\_hlg\_vrl:\*  
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39: em\_hlgo\_hum:\*  
40: em\_hlgo\_mus:\*  
41: em\_hlgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	149	100.0	149	6 AX326745	AX326745 Sequence
2	138	92.6	150	6 AX326746	AX326746 Sequence
3	137	91.9	148	6 AX326744	AX326744 Sequence
4	131	87.9	145	6 AX326743	AX326743 Sequence
5	73.6	49.4	5639	12 CV014122	U14122 Cloning vec
6	71.2	47.8	259	6 A44281	A44281 Sequence 9
7	70.8	47.5	859	11 CNE06EDT	AL394983 T7 end of
8	70.4	47.2	525	5 AF309793	AF309793 Clupea pa
9	70.2	47.1	13558	6 AX287041	AX287041 Sequence
10	70	47.0	424	6 AX284796	AX284796 Sequence
11	70	47.0	2059	12 AT034154	AT034154 Cloning v
12	70	47.0	2850	9 AB035274	AB035274 Homo sapi
13	70	47.0	2958	6 AX247548	AX247548 Sequence
14	70	47.0	2958	12 ARBLKSM	AX2326 pbuescript
15	70	47.0	2958	12 ARBLKSM	AX2326 pbuescript
16	70	47.0	2961	12 ARBLKSM	AX2327 pbuescript
17	70	47.0	2961	12 ARBLKSM	AX2327 pbuescript
18	70	47.0	2964	12 SYNBLSKV	L08784 Bluescribe
19	70	47.0	2964	12 SYNBLSKV	D85525 Cloning vec
20	70	47.0	3306	12 SYNBEN66	AF153422 Cloning v
21	70	47.0	3417	12 AF153422	AF178449 Integrat
22	70	47.0	3485	12 AF178449	U35131 Plasmid pbs
23	70	47.0	4144	12 XXU35131	U35136 Plasmid pbs
24	70	47.0	4267	12 PRS304	U03436 Yeast integ
25	70	47.0	4289	12 PRS306	U03438 Yeast integ
26	70	47.0	4373	12 PRS303	U03435 Yeast integ
27	70	47.0	4443	12 PRS303	AF178452 Integrat
28	70	47.0	4549	12 AF178452	AJ005326 pgAT1(+)
29	70	47.0	4670	12 ASAJ5326	AJ005329 pgAT1(-)
30	70	47.0	4707	12 ASAJ5329	U02374 Cloning vec
31	70	47.0	4768	12 XXU2374	U02061 Cloning vec
32	70	47.0	4768	12 PRS314	U03440 Yeast centr
33	70	47.0	4887	12 PRS316	U03437 Yeast integ
34	70	47.0	4950	12 XXU25060	U03439 Yeast centr
35	70	47.0	4967	12 PRS313	U03436 Yeast integ
36	70	47.0	5144	12 CV023751	U23751 Cloning vec
37	70	47.0	5187	12 U34887	U34887 Yeast integ
38	70	47.0	5228	12 XXU25059	U25059 Cloning vec
39	70	47.0	5504	12 PRS305	U03437 Yeast integ
40	70	47.0	5634	12 CVU14125	U14125 Cloning vec
41	70	47.0	5973	12 AF504908	AF504908 Cloning v
42	70	47.0	6018	12 PRS315	U03441 Yeast centr
43	70	47.0	6340	12 ASAJ5323	AJ005323 pcP1(-) K
44	70	47.0	9655	12 SYNPR8V	AD001531 Cloning v
45	70	47.0	9655	12 SYNPR8V	AD001531 Cloning v

#### ALIGNMENTS

RESULT 1  
AX326745  
LOCUS AX326745 149 bp DNA linear PAT 07-JAN-2002  
DEFINITION Sequence 6 from Patent WO0172995.  
ACCESSION AX326745  
VERSION AX326745.1 GI:18097471  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct.  
artificial sequences.  
REFERENCE  
1 Zauderer, M. and Smith, E.S.  
Methods of producing a library and methods of selecting  
polynucleotides of interest  
Patent: WO 0172995-A 6 04-OCT-2001;  
JOURNAL

UNIVERSITY OF ROCHESTER (US)  
location/Qualifiers  
1. .149  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Nucleotide Sequence of p7.5/ATG2/Lk"  
BASE COUNT 36 a 37 c 39 g 37 t  
ORIGIN

Query Match 100.0%; Score 149; DB 6; Length 149;  
Best Local Similarity 100.0%; Pred. No. 4e-35;  
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCAAAATTTGAAAACCTAGATCTATTATTATTCACGGCGCGCCGACGAGTGCATCCGCC 60  
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QY 61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGCTGCACCTCGAGGGGGGCGCTAAC 120  
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DB 61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGCTGCACCTCGAGGGGGGCGCTAAC 120  
|||||

QY 121 TAACATAATTTGTTTTGTTGGCGCGGCC 149  
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DB 121 TAACATAATTTGTTTTGTTGGCGCGGCC 149  
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RESULT 2  
AX326746 150 bp DNA linear PAT 07-JAN-2002  
DEFINITION Sequence 7 from Patent W00172995.  
ACCESSION AX326746  
VERSION AX326746.1 GI:18097472  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Zauderer, M. and Smith, E.S.  
TITLE Methods of producing a library and methods of selecting polynucleotides of interest  
JOURNAL Patent: WO 0172995-A 7 04-OCT-2001;  
UNIVERSITY OF ROCHESTER (US)  
FEATURES  
source Location/Qualifiers  
1. .150  
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/db\_xref="taxon:32630"  
/note="Nucleotide Sequence of p7.5/ATG3/Lk"  
BASE COUNT 36 a 38 c 39 g 37 t  
ORIGIN

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Best Local Similarity 99.3%; Pred. No. 9.4e-32;  
Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGGCAAAATTTGAAAACCTAGATCTATTATTATTCACGGCGCGCCGACGAGTGCATCCGCC 59  
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QY 60 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGCTGCACCTCGAGGGGGGCGCTAAC 119  
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DB 61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGCTGCACCTCGAGGGGGGCGCTAAC 120  
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QY 120 CTAACTAATTTGTTTTGTTGGCGCGGCC 149  
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DB 121 CTAACTAATTTGTTTTGTTGGCGCGGCC 150  
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RESULT 3  
AX326744 148 bp DNA linear PAT 07-JAN-2002  
DEFINITION Sequence 5 from Patent W00172995.  
ACCESSION AX326744  
VERSION AX326744.1 GI:18097470

KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Zauderer, M. and Smith, E.S.  
TITLE Methods of producing a library and methods of selecting polynucleotides of interest  
JOURNAL Patent: WO 0172995-A 5 04-OCT-2001;  
UNIVERSITY OF ROCHESTER (US)  
FEATURES  
source Location/Qualifiers  
1. .148  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Nucleotide Sequence of p7.5/ATG1/Lk"  
BASE COUNT 35 a 37 c 39 g 37 t  
ORIGIN

Query Match 91.9%; Score 137; DB 6; Length 148;  
Best Local Similarity 99.3%; Pred. No. 1.9e-31;  
Matches 148; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGGCAAAATTTGAAAACCTAGATCTATTATTATTCACGGCGCGCCGACGAGTGCATCCGCC 60  
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DB 1 GGGCAAAATTTGAAAACCTAGATCTATTATTATTCACGGCGCGCCGACGAGTGCATCCGCC 59  
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QY 61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGCTGCACCTCGAGGGGGGCGCTAAC 120  
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DB 60 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGCTGCACCTCGAGGGGGGCGCTAAC 119  
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QY 121 TAACATAATTTGTTTTGTTGGCGCGGCC 149  
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DB 120 TAACATAATTTGTTTTGTTGGCGCGGCC 148  
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RESULT 4  
AX326743 145 bp DNA linear PAT 07-JAN-2002  
DEFINITION Sequence 4 from Patent W00172995.  
ACCESSION AX326743  
VERSION AX326743.1 GI:18097469  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Zauderer, M. and Smith, E.S.  
TITLE Methods of producing a library and methods of selecting polynucleotides of interest  
JOURNAL Patent: WO 0172995-A 4 04-OCT-2001;  
UNIVERSITY OF ROCHESTER (US)  
FEATURES  
source Location/Qualifiers  
1. .145  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Nucleotide Sequence of p7.5/ATG0/Lk"  
BASE COUNT 34 a 37 c 38 g 36 t  
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Query Match 87.9%; Score 131; DB 6; Length 145;  
Best Local Similarity 97.3%; Pred. No. 1.3e-29;  
Matches 145; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 GGGCAAAATTTGAAAACCTAGATCTATTATTATTCACGGCGCGCCGACGAGTGCATCCGCC 60  
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DB 1 GGGCAAAATTTGAAAACCTAGATCTATTATTATTCACGGCGCGCCGACGAGTGCATCCGCC 56  
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QY 61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGCTGCACCTCGAGGGGGGCGCTAAC 120  
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DB 57 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGCTGCACCTCGAGGGGGGCGCTAAC 116  
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QY 121 TAACATAATTTGTTTTGTTGGCGCGGCC 149  
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PUBMED		11152876	
REFERENCE	2 (bases 1 to 859)		
AUTHORS	de Montigny,J., Straub,M., Potier,S., Tekala,F., Dujon,B., Wincker,P., Artiguenave,F. and Souciet,J.		
TITLE	Genomic exploration of the hemiascomycetous yeasts : 8. Zygosaccharomyces rouxii		
JOURNAL	FEMS Lett. 487 (1), 52-55 (2000)		
MEDLINE	20584718		
PUBMED	11152883		
REFERENCE	3 (bases 1 to 859)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-SBP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)		
COMMENT	This STS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert. Location/Qualifiers 1..859 /organism="Zygosaccharomyces rouxii" /strain="CBS 732" /db_xref="taxon:4956" /clone="FARGAA20G08" /clone_lib="AROMA" /note="End : T7"		
FEATURES			
source	1..859		
SIS	258 a 155 c 221 g 222 t 3 others		
BASE COUNT			
ORIGIN			
Query Match	47.5% Score 70.8; DB 11; Length 859;		
Best local similarity	Matches 84; Conservative 0; Mismatches 22; Indels 0; Gaps 0;		
OY	11 TGAAAACATAGATCTATTATTATGTGCAGCGGGCCGCCCATGAGTGCATCCCCGGGGCTGCAGG 70		
DB	730 TGAAGAATACAGTTATTCCTTTCAATCAAGTGCCACAGTAGTAATGATGATCCC CGGGCTGCAGG 789		
OY	71 AATTGATATCACAAGCTTATTCGATACCCTGACCTGAGAGGGGGGCC 116		
DB	790 AATTGATATCAAGCTTATTCGATACCGTCGACCTGAGAGGGGGGCC 835		
RESULT 8			
AF309793/c			
LOCUS	AF309793 525 bp DNA linear VRT 23-JAN-2002		
DEFINITION	Clupea pallasi microsatellite Chai13 sequence.		
VERSION	AF309793		
KEYWORDS	AF309793.1 GI:12060921		
SOURCE	.		
ORGANISM	Clupea pallasi.		
	Clupea pallasi.		
	Euharoptea Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae; Clupea.		
REFERENCE	1 (bases 1 to 525)		
AUTHORS	Miller,K.M., Laboree,K., Schulze,A.D. and Kaukinen,K.H.		
TITLE	Development of microsatellite loci in Pacific herring (Clupea pallasii)		
JOURNAL	Mol. Ecol. Notes 1 (3), 131-132 (2001)		
REFERENCE	2 (bases 1 to 525)		
AUTHORS	Miller,K.M., Laboree,K. and Kaukinen,K.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-OCT-2000) Aquaculture/Genetics, Pacific Biological Station, Hammond Bay Rd., Nanaimo, B.C. V9R 5K6, Canada		
FEATURES	Location/Qualifiers		

source	1..525 /organism="Clupea pallasii" /db_xref="taxon:30724" /clone="Chall3"
repeat_region	1..525 /note="microsatellite Chall3" /rpt_type=tandem
BASE COUNT	130 a 136 c 166 g 93 t
ORIGIN	
Query Match	47.2%; Score 70.4; DB 5; Length 525;
Best Local Similarity	79.8%; Pred. No. 6e-11;
Matches	83; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
OY	31 TTGGCGGCGCCGCATGTGATGCCCGGGCGCAGAAATTGATATCAAGCTTATC 90      c   c   c   c   c   c   c   c   c   c   c   c   c   c    Db 126 TTGCATGTGAGACACCAGCACAGATCCCCCGGGCTGCAGAAATTGATATCAAGCTTATC 67
OY	91 GATACCGTCGACCTCGAGGGGGGCGCTTAACAATAAATTGTT 134      c   c   c   c   c   c   c   c   c   c   c   c   c   c    Db 66 GATACCGTCGACCTCGAGGGGGGCGCGCCAGTACCAGCTTTGTT 23
RESULT 9	
LOCUS	AX287041 13558 bp DNA linear PAT 21-NOV-2001
DEFINITION	Sequence 5 from Patent WO0181623.
ACCESSION	AX287041
VERSION	AX287041.1 GI:17049037
KEYWORDS	house mouse. Mus musculus
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 Goeltz,B., Kammandel,B., Kuner,R., Scheek,S. and Hjemisch,H. Novel neuronally expressed protein and use thereof Patent: WO 0181623-A 5 01-NOV-2001;
AUTHORS	BASF-LYNX Bioscience AG (DE)
TITLE	Location/Qualifiers
JOURNAL	1..13558 /organism="Mus musculus" /db_xref="taxon:10090"
FEATURES	
source	
BASE COUNT	2936 a 3419 c 3606 g 3544 t 53 others
ORIGIN	
Query Match	47.1%; Score 70.2; DB 6; Length 13558;
Best Local Similarity	96.0%; Pred. No. 1.1e-10;
Matches	72; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY	42 CGCCATGAGTGATCCCCCGGCTGCAGAAATTGATATCAAGCTTATCGATACCGTGA 101      t   t   t   t   t   t   t   t   t   t   t   t   t   t    Db 13479 CCGAAGCGGTGATCCCCCGGGCTGCAGAAATTGATATCAAGCTTATCGATACCGTGA 13558
OY	102 CCTCGAGGGGGGGCC 116      t   t   t   t   t   t   t   t   t   t   t   t   t   t    Db 13539 CCTCGAGGGGGGGCC 13553
RESULT 10	
LOCUS	AX284796 424 bp DNA linear PAT 20-NOV-2001
DEFINITION	Sequence 601 from Patent WO0179556.
ACCESSION	AX284796
VERSION	AX284796.1 GI:17045484
KEYWORDS	human. Homo sapiens
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
ORGANISM	Lillie,J., Brown,J.L., Bolt,A. and van Huuffel,C. Novel genes, compositions and methods for the identification,
AUTHORS	
TITLE	



Assessment, prevention, and therapy of human cancers  
Patent: WO 0179556-A 601.25-OCT-2001;  
Millennium Predictive Medicine, Inc. (US)  
Location/Qualifiers  
1. .424  
/db\_xref="taxon:9606"  
/organism="Homo sapiens"  
BASE COUNT 87 a 134 c 118 g 85 t  
ORIGIN

Query Match  
Best Local Similarity 47.0%; Score 70; DB 6; Length 424;  
Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 49 AGTGGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108  
|||||  
Db 105 AGTGGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 46  
|||||  
OY 109 GGGGGCCCTAAGTAACTAATTTGTT 134  
|||||  
Db 45 GGGGGCCCGGTACCCAGCTTTGTT 20

RESULT 11  
AY034154/c 2059 bp DNA Circular SYN 23-JUL-2001  
LOCUS Cloning vector PIDM4, complete sequence.  
ACCESSION AY034154  
VERSION AY034154.1 GI:14324126  
KEYWORDS  
SOURCE Cloning vector PIDM4.  
ORGANISM Cloning vector PIDM4  
artificial sequences; vectors.  
REFERENCE 1 (bases 1 to 2059)  
AUTHORS Hamilton,H.L., Schwartz,K.J. and Dillard,J.P.  
TITLE Insertion-duplication mutagenesis of neisseria: use in  
characterization of DNA transfer genes in the gonococcal genetic  
island  
JOURNAL J. Bacteriol. 183 (16), 4718-4726 (2001)  
MEDLINE 21359313  
PIRME 11466274  
2 (bases 1 to 2059)  
AUTHORS Hamilton,H.L., Schwartz,K.J. and Dillard,J.P.  
TITLE Direct Submission  
JOURNAL Submitted (11-MAY-2001) Medical Microbiology & Immunology,  
University of Wisconsin-Madison, 1300 University Avenue, Madison,  
WI 53706, USA  
FEATURES  
source Location/Qualifiers  
1. .2059  
/organism="Cloning vector PIDM4"  
/db\_xref="taxon:161273"  
/note="for insertion-duplication mutagenesis in Neisseria"  
40. .59  
/note="T3"  
promoter complement(187. .204)  
/note="T7"  
277. .311  
gene complement(310. .1113)  
/gene="ermC"  
CDS complement(310. .1044)  
/gene="ermC"  
/codon\_start=1  
/transl\_table=11  
/product="ermC"  
/protein\_id="AAK58461.1"  
/db\_xref="GI:14324127"  
/translation="MNEKNIKHSQNFITSKNIDKIMTNI RLNEHNDIFEIGSGKGF  
TELVORCNFVTAIEIDHKLKTEENKLVHDHNFVYLNKDILQFKPKNOSYKIEGFI  
PYNISYDIIRKIVFSDIADIEIYLIVYGAFAKRLNTRKALFLMAEVDISITSWYPR  
EYFHPKRYNSSLIRLNRRKRSRSHRDKQYNFVAKWVKEIKKLTFTKNQFNLSLKH  
AGIDDLNNTSFEPLSLFNSYKLFNK"  
complement(1051. .1054)  
/gene="ermC"  
RBS

-10-signal complement(1086. .1091)  
/gene="ermC"  
-35-signal complement(1108. .1113)  
/gene="ermC"  
misc-feature 1130. .1139  
/note="DNA uptake sequence (DUS)"  
misc-feature complement(1145. .1154)  
/note="DNA uptake sequence (DUS)"  
misc\_RNA complement(1276. .1976)  
/note="RNA IT"  
rep\_origin complement(1422. .1423)  
-35-signal 1830. .1835  
-10-signal 1854. .1859  
misc\_RNA 1866. .1973  
/note="RNA IT"  
-10-signal complement(1984. .1989)  
-35-signal complement(2007. .2012)  
BASE COUNT 566 a 452 c 424 g 617 t  
ORIGIN

Query Match  
Best Local Similarity 47.0%; Score 70; DB 12; Length 2059;  
Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 49 AGTGGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108  
|||||  
Db 144 AGTGGATCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 85  
|||||  
OY 109 GGGGGCCCTAAGTAACTAATTTGTT 134  
|||||  
Db 84 GGGGGCCCGGTACCCAGCTTTGTT 59

RESULT 12  
AB035274 2890 bp mRNA linear PRI 12-JUL-2000  
LOCUS Homo sapiens mRNA for postreplication repair protein hRAD18p,  
complete cds.  
ACCESSION AB035274  
VERSION AB035274.1 GI:8980616  
KEYWORDS  
SOURCE Homo sapiens placenta cDNA to mRNA.  
ORGANISM Homo sapiens  
REFERENCE 1 (sites)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
TITLE Tateshi,S., Sakuraba,Y., Masuyama,S., Inoue,H. and Yamazumi,M.  
repair and hypersensitivity to multiple mutagens  
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7927-7932 (2000)  
JOURNAL 20345089  
2 (bases 1 to 2890)  
AUTHORS Tateshi,S., Yamazumi,M. and Inoue,H.  
TITLE Direct Submission  
JOURNAL Submitted (26-NOV-1999) Satoshi Tateshi, Kumamoto University,  
Institute of Molecular Embryology, Honjoji 4-24-1, Kumamoto,  
Kumamoto 862-0976, Japan (E-mail:tate@ipo.kumamoto-u.ac.jp,  
tel:81-096-373-6602, Fax:81-096-373-6604)  
FEATURES  
source Location/Qualifiers  
1. .2890  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="3"  
/tissue\_type="Placenta"  
1. .2890  
/gene="hRAD18"  
126. .1613  
CDS /gene="hRAD18"  
/note="RING-zinc-finger protein"  
/codon\_start=1  
/product="postreplication repair protein hRAD18p"  
/protein\_id="BAA99284.1"  
/db\_xref="GI:8980617"

/translation="MDSIAESRMPGGLAVKTTIDDLRCGICFCEFNINAMITIPCCSHN  
YCSLICIRFELSYKTQCPVCVTEPPDLKNNRIIDELIKSINFRNHLIOTALSPK  
SPASSSSKNLAVKYTPVARSOSLKGSRMDNPLIRMSSTSELLIKERKSFSPQ  
KEASPAARTKEEVEEIPADPSEAKREPSTSLKQVTVDCPVGVNIPESHINK  
HDSCTLSREEKESLSVHKRKPLPKTVYMLSDRLKRLKEHSLIQGNKOOLIK  
RHOEFVHMVNAOCALHPKSAEIVQELIENTEKTMRLEASKLNSVVFVKDTERE  
IDELISKYRKHKHSPFOILVPOARKGYKIKAGMSQKTVITRKEDESTERKSSVGMGE  
DMNISTVNFSSKSLDSEEPLEPDRREESSCIDIQEVLSSSESSSCSSSSDIIRDL  
LEEFEAWBSHKNIDQDTEISPRONRRTRAEASAEIPEPRNRRN"

BASE COUNT 916 a 585 c 601 g 788 t

ORIGIN

Query Match 47.0%; Score 70; DB 9; Length 2890;  
Best Local Similarity 88.4%; Pred. No. 1e-10; Indels 0; Gaps 0;  
Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 49 AGTGATGCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108  
|||||  
DB 2741 AGTGATGCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 2800  
|||||

OY 109 GGGGGGCTTAACCTAATTTTGT 134  
|||||

DB 2801 GGGGGGCTTAACCTAATTTTGT 2826  
|||||

RESULT 13  
AX247548 2958 bp DNA linear PAT 28-SEP-2001  
LOCUS AX247548  
DEFINITION Sequence 1 from Patent WO0166775.  
ACCESSION AX247548  
VERSION AX247548.1 GI:15862240  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 2958)  
AUTHORS Evans,D.H., Willer,D.O. and Yao,X.D.  
TITLE Dna joining method  
JOURNAL Patent: WO 0166775-A 1 13-SEP-2001;  
University of Guelph (CA)  
FEATURES  
source  
Location/Qualifiers  
1..2958  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="pDM101"

BASE COUNT 748 a 735 c 752 g 723 t

ORIGIN

Query Match 47.0%; Score 70; DB 6; Length 2958;  
Best Local Similarity 88.4%; Pred. No. 1e-10;  
Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 49 AGTGATGCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108  
|||||  
DB 683 AGTGATGCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 742  
|||||

OY 109 GGGGGGCTTAACCTAATTTTGT 134  
|||||

DB 743 GGGGGGCTTAACCTAATTTTGT 768  
|||||

RESULT 14  
ARBLKSM 2958 bp DNA circular SYN 29-JAN-2002  
LOCUS ARBLKSM  
DEFINITION pluescript KS(-) vector DNA, phagemid excised from lambda ZAP.  
ACCESSION X52326  
VERSION X52326.1 GI:58064  
KEYWORDS artificial sequence; cloning vector; expression vector; vector.  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Short,J.M., Fernandez,J.M., Sorge,J.A. and Huse,W.D.

TITLE Lambda ZAP: a bacteriophage lambda expression vector with in vivo  
JOURNAL excision properties  
MEDLINE Nucleic Acids Res. 16 (15), 7583-7600 (1988)  
88319944  
2970625  
PUBMED  
REFERENCE  
AUTHORS Alting-Mees,M.A. and Short,J.M.  
TITLE pluescript II: gene mapping vectors  
JOURNAL Nucleic Acids Res. 17 (22), 9494 (1989)  
90067967  
MEDLINE  
PUBMED 2557794  
REFERENCE  
AUTHORS 3 (bases 1 to 2958)  
Thomas,E.A.  
TITLE Direct Submission  
JOURNAL Submitted (20-FEB-1990) Thomas E.A., Stratagene Clonin Systems,  
11099 North Torrey Pines Rd., La Jolla, CA 92037, USA  
1..2958  
Location/Qualifiers  
1..2958  
/organism="synthetic construct"  
/db\_xref="taxon:32630"

misc\_feature 1..2958  
BASE COUNT 708 a 754 c 731 g 765 t

ORIGIN

Query Match 47.0%; Score 70; DB 12; Length 2958;  
Best Local Similarity 88.4%; Pred. No. 1e-10;  
Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 49 AGTGATGCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108  
|||||  
DB 686 AGTGATGCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 745  
|||||

OY 109 GGGGGGCTTAACCTAATTTTGT 134  
|||||

DB 746 GGGGGGCTTAACCTAATTTTGT 771  
|||||

RESULT 15  
ARBLKSP 2958 bp DNA circular SYN 29-JAN-2002  
LOCUS ARBLKSP  
DEFINITION pluescript KS(+) vector DNA, phagemid excised from lambda ZAP.  
ACCESSION X52331  
VERSION X52331.1 GI:58065  
KEYWORDS artificial sequence; cloning vector; expression vector; vector.  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1  
AUTHORS Short,J.M., Fernandez,J.M., Sorge,J.A. and Huse,W.D.  
TITLE Lambda ZAP: a bacteriophage lambda expression vector with in vivo  
JOURNAL Nucleic Acids Res. 16 (15), 7583-7600 (1988)  
88319944  
PUBMED 2970625  
REFERENCE  
AUTHORS 2  
Alting-Mees,M.A. and Short,J.M.  
TITLE pluescript II: gene mapping vectors  
JOURNAL Nucleic Acids Res. 17 (22), 9494 (1989)  
90067967  
MEDLINE  
PUBMED 2557794  
REFERENCE  
AUTHORS 3  
Lampe,D.J., Grant,T.E. and Robertson,H.M.  
TITLE Factors affecting transposition of the Himari mariner transposon in  
JOURNAL vitro  
MEDLINE Nucleic Acids Res. 17 (1), 179-187 (1998)  
98250682  
PUBMED 9584095  
REFERENCE  
AUTHORS 4 (bases 1 to 2958)  
Thomas,E.A.  
TITLE Direct Submission  
JOURNAL Submitted (20-FEB-1990) Thomas E.A., Stratagene Clonin Systems,  
11099 North Torrey Pines Rd., La Jolla, CA 92037, USA

FEATURES : Location/Qualifiers  
source 1..2958 /organism="synthetic construct"  
misc\_feature 1..2958 /db\_xref="taxon:32630"  
BASE COUNT 749 a 734 c 751 g 724 t  
ORIGIN  
Query Match 47.0%; Score 70; DB 12; Length 2958;  
Best Local Similarity 88.4%; Pred. No. 1e-10; Mismatches 10; Indels 0; Gaps 0;  
Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 49 AGTGGATCCCCGGGCTGCGAGATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108  
|||||  
DB 686 AGTGGATCCCCGGGCTGCGAGATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 745  
|||||  
QY 109 GGGGGGCTTAACCTAATTTGTT 134  
|||||  
DB 746 GGGGGGCTTAACCTAATTTGTT 771  
|||||

Search completed: November 10, 2002, 06:53:02  
Job time : 730.448 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:42:15 ; Search time 1341 Seconds

(without alignments)  
1799.499 Million cell updates/sec

Title: US-08-935-377-8

Perfect score: 149  
Sequence: 1 GCCCAAAATGAAAACTA.....TTGTTTGTGCGCCGCCGCC 149

Scoring table: IDENTITY\_NUC  
Gapop 10.0 ; Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estlmu:\*  
5: em\_estlov:\*  
6: em\_estlpl:\*  
7: em\_estro:\*  
8: em\_hcc:\*  
9: gb\_estl1:\*  
10: gb\_estl2:\*  
11: gb\_hcc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estlun:\*  
16: em\_estlun:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76.4	51.3	891	14	B0140386
2	73	49.0	182	13	B1306115
3	73	49.0	793	14	B0143916
4	71	47.7	682	17	A0074693
5	70.8	47.5	804	14	B0158468
6	70.4	47.2	128	17	CNS07GJ4

C	7	70.4	47.2	182	13	B1305962	B1305962	NL_2_K23
C	8	70.4	47.2	186	13	B1305695	B1305695	NL_1_G23
C	9	70	47.0	162	10	BE428068	BE428068	MTD002.H1
C	10	70	47.0	390	9	AU234451	AU234451	AU234451
C	11	70	47.0	400	9	AU278852	AU278852	AU278852
C	12	70	47.0	864	17	A0937400	A0937400	NB2_011.H
C	13	69.8	46.8	175	13	B1306167	B1306167	NL_3_J08
C	14	69.8	46.8	182	13	B1306149	B1306149	NL_3_J07
C	15	69.8	46.8	182	13	B1306159	B1306159	NL_3_K12
C	16	69.8	46.8	182	13	B1306178	B1306178	NL_3_K05
C	17	69.8	46.8	182	13	B1306180	B1306180	NL_3_K07
C	18	69.8	46.8	175	14	B0155148	B0155148	NF076G11
C	19	69.2	46.4	727	10	AM682573	AM682573	EST01439
C	20	69.2	46.4	912	17	CNS06005	CNS06005	AL415767.T7 end of
C	21	69	46.3	295	10	BE428455	BE428455	MTD007.C0
C	22	68.6	46.0	608	17	A0009167	A0009167	CIT-HSP-2
C	23	68.6	46.0	212	17	CNS060D1G	CNS060D1G	AL393854.T7 end of
C	24	68.6	46.0	829	17	A0937397	A0937397	NB2_006.H
C	25	68.4	45.9	528	17	B63688	B63688	CIT978SK-A-
C	26	68.2	45.8	207	17	CNS060DNG	CNS060DNG	AL394034.T7 end of
C	27	68.2	45.8	728	10	AM682547	AM682547	EST01410
C	28	68	45.6	107	13	BM398556	BM398556	5009-0-47
C	29	68	45.6	108	10	BE492551	BE492551	WHE0554.C
C	30	68	45.6	108	17	B54292	B54292	CIT-HSP-201
C	31	68	45.6	124	10	AM914179	AM914179	EST345483
C	32	68	45.6	141	9	AU037147	AU037147	AU037147
C	33	68	45.6	141	17	B95279	B95279	CIT-HSP-217
C	34	68	45.6	144	17	B80294	B80294	CIT-HSP-204
C	35	68	45.6	157	12	BF281431	BF281431	EST446022
C	36	68	45.6	169	13	B1306719	B1306719	NL_5_N23
C	37	68	45.6	169	17	AQ013235	AQ013235	CIT-HSP-2
C	38	68	45.6	175	17	AQ041198	AQ041198	CIT-HSP-2
C	39	68	45.6	180	13	B1306345	B1306345	NL_4_E10
C	40	68	45.6	181	13	B1305488	B1305488	NL_0_B05
C	41	68	45.6	181	13	B1305783	B1305783	NL_1_L10
C	42	68	45.6	182	13	B1305555	B1305555	NL_0_J13
C	43	68	45.6	184	13	B1305662	B1305662	NL_1_E24
C	44	68	45.6	184	13	B1305671	B1305671	NL_1_F13
C	45	68	45.6	208	14	BM730642	BM730642	1h47d11.x

#### ALIGNMENTS

RESULT 1  
B0140386  
LOCUS  
DEFINITION  
NP035A10PH1081 Phoma-infected Medicago truncatula cDNA clone  
ACCESSION  
B0140386  
VERSION  
B0140386.1 GI:20276512  
KEYWORDS  
EST.  
SOURCE  
barrel medic.  
ORGANISM  
Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;  
Medicago.  
REFERENCE  
1 (bases 1 to 891)  
Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,  
Gonzales,R.A., Bell,C.J., Imman,J.T., Waugh,M.E., Sullivan,J.P.,  
May,G.D. and Palva,N.L.  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
Medicago truncatula Phoma-infected library  
Unpublished (2002)  
CONTACT  
Contact: Palva NL  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel.: 580 221 7317  
Fax: 580 221 7380  
Email: nlpalva@noble.org  
Insert Length: 891 Std Error: 0.00

JOURNAL  
COMMENT

Plate: 035 row: A column: 10  
Seq primer: TCACACAGGAACAGCTATGAC.  
Location/Qualifiers

# FEATURES

## SOURCE

1. 891  
/organism="Medicago truncatula"  
/db\_xref="taxon:3880"  
/clone="NF035A10PH"  
/issue\_1lb="Phoma-infected"  
/tissue\_type="leaf"

/dev\_stage="Pathogen-induced, young trifoliolate"  
/note="Vector: Bluescript SK(-); Young trifoliolate leaves of Medicago truncatula were excised and dip-inoculated in a spore suspension of Phoma medicaginis, and incubated in humid dishes. Pools of leaves were harvested at 0, 15, and 30 minutes and 1, 2, 3, 6, 14, 24, 48, 72, and 96 hours, and used to prepare total RNA. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using Exassist helper phage and the E. coli strain XL1-Blue MR<sup>+</sup> (Stratagene). Excised plasmids were plated using SOUR cells."

BASE COUNT 188 a 151 c 64 g 224 t 264 others  
ORIGIN

Query Match 51.3%; Score 76.4; DB 14; Length 891;  
Best Local Similarity 87.9%; Pred. No. 2.7e-15;  
Matches 80; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 49 AGTGGATCCCCGGGCGCTGACGAAATTCGATTCAGCTTATCGATTACCGCTCGAG 108  
|||||  
Db 83 AGTGATCCCCCGGCGCTGACGAAATTCGATTCAGCTTATCGATTACCGCTCGAG 142  
QY 109 GGGGGCGCTACTACTAATTTTGTGTTTGT 139  
|||||  
Db 143 GGGGGCGCGCTANCTAATTTTNTCTATNT 173

RESULT 2  
BI306115/c 182 bp mRNA linear EST 20-JUL-2001  
LOCUS NL\_3\_G09 Drought stress (leaf) Oryza sativa cDNA clone NL\_3\_G09 3',  
DEFINITION mRNA sequence.  
ACCESSION BI306115  
VERSION BI306115.1 GI:14981437  
KEYWORDS EST.  
SOURCE Oryza sativa.  
ORGANISM Oryza sativa.  
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehmatoidae; Oryzaceae; Oryza.  
1 (bases 1 to 182)  
Reddy,A.R., Ramakrishna,W., Chandrasekhar,A., Nagabushan,I.,  
Ravindrababu,P. and Bennetzen,J.L.  
Novel EST enrichment with normalized cDNA libraries from drought  
stressed rice (Oryza sativa L.cv Nagina 22)  
Unpublished (2001)  
Contact: Reddy AR  
Department of Plant Sciences, School of Life Sciences  
University of Hyderabad  
P.O. Central University, Hyderabad-500 046, A.P, India  
Tel: 0091-40-3010265  
Fax: 0091-40-3010145  
Email: arjuls@uohyd.ernet.in  
Insert Length: 182 Std Error: 0.00  
Plate: 3 row: G column: 09  
Seq primer: GTAAACGACGCGCAGC.  
Location/Qualifiers

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Unpublished (2001)

Contact: Reddy AR  
Department of Plant Sciences, School of Life Sciences  
University of Hyderabad  
P.O. Central University, Hyderabad-500 046, A.P, India  
Tel: 0091-40-3010265  
Fax: 0091-40-3010145  
Email: arjuls@uohyd.ernet.in  
Insert Length: 182 Std Error: 0.00  
Plate: 3 row: G column: 09  
Seq primer: GTAAACGACGCGCAGC.  
Location/Qualifiers

FEATURES  
source  
/organism="Oryza sativa"

/cultivar="Nagina 22 (indica sub sp)"  
/db\_xref="taxon:4530"  
/clone="NL\_3\_G09"  
/issue\_1lb="Drought stress (leaf)"  
/tissue\_type="Entire leaf tissue"  
/dev\_stage="35 day-old seedlings"  
/note="Organ: leaf; Vector: T773Pac; ESTs from normalized  
leaf cDNA library from drought stressed seedlings"

BASE COUNT 34 a 47 c 53 g 48 t  
ORIGIN

Query Match 49.0%; Score 73; DB 13; Length 182;  
Best Local Similarity 93.8%; Pred. No. 3.4e-14;  
Matches 76; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 49 AGTGATCCCCGGGCGCTGACGAAATTCGATTCAGCTTATCGATTACCGCTCGAG 108  
|||||  
Db 108 AGTGATCCCCCGGCGCTGACGAAATTCGATTCAGCTTATCGATTACCGCTCGAG 49

QY 109 GGGGGCGCTACTACTAATTTTGTGTTTGT 129  
|||||  
Db 48 GGGGGCGCGAGTACCCCAATT 28

RESULT 3  
B0143916 793 bp mRNA linear EST 24-APR-2002  
LOCUS NF038H04D1F1041 Drought Medicago truncatula cDNA clone NF038H04D  
DEFINITION 5', mRNA sequence.  
ACCESSION B0143916  
VERSION B0143916.1 GI:20280975  
KEYWORDS EST.  
SOURCE barrel medic.  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabiales; Fabaceae; Papilionoideae; Trifoliaceae;  
Medicago.  
1 (bases 1 to 793)  
Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,  
Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.  
Expressed Sequence tags from the Samuel Roberts Noble Foundation  
Medicago truncatula drought library  
Unpublished (2000)  
Contact: May GD  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7391  
Fax: 580 221 7380  
Email: gdmay@noble.org  
Insert Length: 793 Std Error: 0.00  
Plate: 038 row: H column: 04  
Seq primer: TCACACAGGAACAGCTATGAC.  
Location/Qualifiers

# FEATURES

## source

1. 793  
/organism="Medicago truncatula"  
/db\_xref="taxon:3880"  
/clone="NF038H04D"  
/issue\_1lb="Drought"  
/tissue\_type="Plantlets"  
/dev\_stage="Pooled timepoints"  
/note="Vector: Lambda zap; Contains a mixture of entire  
plantlets harvested in a series of days-post-watering  
timepoints."

BASE COUNT 217 a 203 c 205 g 168 t  
ORIGIN

Query Match 49.0%; Score 73; DB 14; Length 793;  
Best Local Similarity 93.8%; Pred. No. 3.9e-14;  
Matches 76; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 49 AGTGATCCCCGGGCGCTGACGAAATTCGATTCAGCTTATCGATTACCGCTCGAG 108

```

Db      84  ACTGATCCCGGGGCTGAGAAATTCGATATCAAGCTTATCGATACCTGCAG 143
Qy      109 GGGGGGCTAACTAAT 129
Db      144 GGGGGGCGCCGACTACCAAT 164

RESULT 4
A0074693/c  A0074693  682 bp  DNA  linear  GSS 20-AUG-1998
LOCUS      CIT-HSP-2301L23.TF CIT-HSP Homo sapiens genomic clone 2301L23, DNA
DEFINITION
ACCESSION  A0074693
VERSION    A0074693.1 GI:3436811
KEYWORDS   GSS.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 682)
            Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
            Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
            Venter,J.C.
            Use of a random human BAC End Sequence Database for Sequence-Ready
            Map Building
            Unpublished (1998)
JOURNAL    Contact: Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: mdadams@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13-21
            Class: BAC ends.

FEATURES
    source             Location/Qualifiers
                        1..682
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="2301L23"
                        /clone_1lb="CIT-HSP"
                        /sex="Male"
                        /cell_type="Sperm"
                        /note="Vector: pbelOBAC11; Site_1: HindIII; Site_2:
                        HindIII"

BASE COUNT  156 a 187 c 187 g 151 t 1 others
ORIGIN
Query Match 47.7%; Score 71; DB 17; Length 682;
Best Local Similarity 93.7%; Pred. NO. 1.9e-13;
Matches 74; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 49 AGTGATCCCCCGGCTGAGAAATTCGATATCAAGCTTATCGATACCTGCAG 108
Db 79 AGTGATCCCCCGGCTGAGAAATTCGATATCAAGCTTATCGATACCTGCAG 20

Qy 109 GGGGGGCTAACTA 127
Db 19 GGGGGGCGCCGACTACCA 1

RESULT 5
B0158468 804 bp mRNA linear EST 24-APR-2002
LOCUS     NF058H09PL1078 Phosphate starved leaf Medicago truncatula cDNA
DEFINITION
ACCESSION B0158468
VERSION    B0158468.1 GI:20295525
KEYWORDS   EST.

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```

SOURCE      barrel medic.
ORGANISM    Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
            Medicago.
            1 (bases 1 to 804)
REFERENCE   Liu,J., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores
            ,H.R., Inman,J.T., Weller,J.W., May,G.D. and Harrison,M.J.
            Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula phosphate-starved leaf library
JOURNAL    Unpublished (2000)
COMMENT     Contact: Harrison MJ
            Plant Biology Division
            The Samuel Roberts Noble Foundation
            2510 Sam Noble Parkway, Ardmore, OK 73402, USA
            Tel: 580 221 7325
            Fax: 580 221 7380
            Email: mjharrison@noble.org
            Insert length: 804 Std Error: 0.00
            Plate: 058 row: H column: 09
            Seq primer: TCACACGAGAACACGCTATGAC.
            Location/Qualifiers
            1..804
            /organism="Medicago truncatula"
            /db_xref="taxon:3880"
            /clone="NF058H09PL"
            /clone_1lb="Phosphate starved leaf"
            /tissue_type="leaf"
            /dev_stage="trifoliolate"
            /note="Vector: lambda Zap. At the trifoliolate stage, M.
            truncatula plants were transplanted to phosphate-free sand
            and grown for a further 30 days. During this 30 day
            period, the plants were fertilized twice weekly with 1/2
            Hoaglands solution containing only 20uM potassium
            phosphate. RNA was prepared from above ground tissues."

BASE COUNT  215 a 202 c 181 g 165 t 41 others
ORIGIN
Query Match 47.5%; Score 70.8; DB 14; Length 804;
Best Local Similarity 89.3%; Pred. NO. 2.2e-13;
Matches 75; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 49 AGTGATCCCCCGGCTGAGAAATTCGATATCAAGCTTATCGATACCTGCAG 108
Db 81 AGTGATCCCCCGGCTGAGAAATTCGATATCAAGCTTATCGATACCTGCAG 140

Qy 109 GGGGGGCTAACTAATTTG 132
Db 141 GGGGGGCGCTGATCCCAATTCG 164

RESULT 6
CNS07GJ4 128 bp DNA linear GSS 02-OCT-2001
LOCUS     CNS07GJ4
DEFINITION
            Anopheles gambiae GSS T7 end of clone 20K20 of library NotreDame1
            from strain PEST of Anopheles gambiae (African malaria mosquito),
            genomic survey sequence.
ACCESSION  AL609826
VERSION    AL609826.1 GI:15916011
KEYWORDS   GSS.
SOURCE     African malaria mosquito.
ORGANISM   Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
            Anopheles.
            1 (bases 1 to 128)
REFERENCE  1
            Genoscope.
            Direct Submission
            Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage :
            BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - web : www.genoscope.cns.fr)
            2 (bases 1 to 128)

```





LOCUS BE428068 162 bp mRNA linear EST 26-JUL-2000  
 DEFINITION MTD002.H10F90615 ITEC MTD Durum wheat Root Library Triticum  
 turgidum subsp. durum cDNA clone MTD002.H10, mRNA sequence.  
 ACCESSION BE428068  
 VERSION BE428068.1 GI:9425911  
 KEYWORDS  
 SOURCE EST.  
 ORGANISM Triticum turgidum subsp. durum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae  
 ; Triticaceae; Triticum.  
 1 (bases 1 to 162)  
 Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier  
 S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,  
 Hermann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,  
 Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,  
 Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,  
 Sorrells,M., Warburton,M. and Weizel,G.  
 International Triticaceae EST Cooperative (ITEC): Production of  
 Expressed Sequence Tags for Species of the Triticaceae  
 Unpublished (2000)  
 JOURNAL Contact: Joudrier P  
 INRA, unite de Biochimie et Biologie Molculaire des Cereales  
 2, Place VIALA, 34060 Montpellier cedex 01 FRANCE  
 Tel: 33 4 99 61 23 84  
 Fax: 33 4 99 61 23 48  
 Email: joudrier@enscm.inra.fr  
 International Triticaceae EST Cooperative (ITEC)  
 http://wheat.pw.usda.gov/genome.  
 Location/Qualifiers  
 1. 162  
 /organism="Triticum turgidum subsp. durum"  
 /cultivar="Siliiana"  
 /db\_xref="taxon:4567"  
 /clone\_1id="MTD002.H10"  
 /clone\_1lb="ITEC MTD Durum Wheat Root Library"  
 /tissue\_type="root"  
 /dev\_stage="3-day-old seedling, water-stressed"  
 /note="vector: pSPORT1; T7 primers used. See pSPORT1  
 polylinker site. 0.3-2.0 kbp average insert size."  
 BASE COUNT 28 a 42 c 49 g 43 t  
 ORIGIN  
 Query Match 47.0%; Score 70; DB 10; Length 162;  
 Best Local Similarity 88.4%; Pred. No. 3.6e-13;  
 Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 Oy 49 AGTGATCCCCGGGCTGCAGAAATTCAGATTATCGATACCGTCGACCTCGAG 108  
 |||||||  
 Db 23 AGTGATCCCCGGGCTGCAGAAATTCAGATTATCGATACCGTCGACCTCGAG 82  
 |||||||  
 Oy 109 GGGGGCCCTAACCTAATTTGTT 134  
 |||||||  
 Db 83 GGGGGCCCGGTACCACTTTGTT 108  
 |||||||  
 RESULT 10  
 AUC34451 390 bp mRNA linear EST 21-SEP-2001  
 LOCUS AUC34451 Bovine placenta cDNA Bos taurus CDNA Cln1153 3',  
 DEFINITION mRNA sequence.  
 ACCESSION AUC34451  
 VERSION AUC34451.1 GI:15719669  
 KEYWORDS  
 SOURCE EST.  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 390)  
 Gohma,H., Lejukole,H.Y., Taniguchi,Y., Yamada,T., Akagi,S., Yasue  
 H. and Sasaki,Y.  
 Analysis of expressed sequence tags from a cDNA library of bovine

JOURNAL placenta  
 COMMENT Unpublished (2001)  
 Contact: Takahisa Yamada  
 Graduate School of Agriculture  
 Kyoto University  
 Sakyo-ku, Kitashirakawa, Kyoto, Kyoto 606-8502, Japan  
 Tel: 81-75-753-6323  
 Fax: 81-75-753-6340  
 Email: tyamada@kans.jkns.kais.kyoto-u.ac.j  
 This clone was obtained from a 3' end cDNA library.  
 Location/Qualifiers  
 1. 390  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone\_1lb="Bovine placenta cDNA"  
 /tissue\_type="placenta"  
 /note="vector: pUC18 Sma I/BAP"  
 BASE COUNT 113 a 77 c 72 g 128 t  
 ORIGIN  
 Query Match 47.0%; Score 70; DB 9; Length 390;  
 Best Local Similarity 88.4%; Pred. No. 3.9e-13;  
 Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 Oy 49 AGTGATCCCCGGGCTGCAGAAATTCAGATTATCGATACCGTCGACCTCGAG 108  
 |||||||  
 Db 299 AGTGATCCCCGGGCTGCAGAAATTCAGATTATCGATACCGTCGACCTCGAG 358  
 |||||||  
 Oy 109 GGGGGCCCTAACCTAATTTGTT 134  
 |||||||  
 Db 359 GGGGGCCCGGTACCACTTTGTT 384  
 |||||||  
 RESULT 11  
 AUC278852/c 400 bp mRNA linear EST 02-JUL-2002  
 LOCUS AUC278852 Cloned bovine placenta cDNA Bos taurus CDNA clone  
 DEFINITION placenta1153 3', mRNA sequence.  
 ACCESSION AUC278852  
 VERSION AUC278852.1 GI:21682162  
 KEYWORDS  
 SOURCE EST.  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 400)  
 Oishi,M., Yamada,T., Goma,H., Lejukole,H.Y., Taniguchi,Y. and  
 Sasaki,Y.  
 EST analysis of cloned bovine fetus and placenta  
 Unpublished (2002)  
 Contact: Masahito Oishi  
 Graduate School of Agriculture  
 Kyoto University  
 Sakyo-ku Kitashirakawa, Kyoto, Kyoto 606-8502, Japan  
 Tel: 81-75-753-6331  
 Fax: 81-75-753-6340  
 Email: oishi@kans.jkns.kais.kyoto-u.ac.jp.  
 Location/Qualifiers  
 1. 400  
 /organism="Bos taurus"  
 /db\_xref="taxon:9913"  
 /clone\_1lb="placenta1153"  
 /clone\_1lb="Cloned bovine placenta cDNA"  
 /dev\_stage="60 embryonic day"  
 /note="Organ: ovary; Vector: pGEM-T Easy; Randomly cloned  
 third differential products (Dp3) of a Representative  
 Differential Analysis (RDA) with bovine corpus luteum as  
 tester tissue and skeletal muscle as driver."  
 BASE COUNT 133 a 73 c 79 g 115 t  
 ORIGIN

Query Match 47.0%; Score 70; DB 9; Length 400;  
 Best Local Similarity 88.4%; Pred. No. 3.9e-13;  
 Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 49 AGTGATCCCCCGGCTGCAGAAATGCATCAAGCTTATCGATACCGTCGACCTCGAG 108  
 |||||  
 DB 92 AGTGATCCCCCGGCTGCAGAAATGCATCAAGCTTATCGATACCGTCGACCTCGAG 33  
 |||||

QY 109 GGGGGGCTTAACCTAATTTTGT 134  
 |||||  
 DB 32 GGGGGGCTTAACCTAATTTTGT 7  
 |||||

RESULT 12  
 LOCUS AO937400/c 864 bp DNA linear GSS 23-AUG-2000  
 DEFINITION N82-011 Human NotI clones Homo sapiens genomic, DNA sequence.  
 ACCESSION AO937400  
 VERSION AO937400.1 GI:7213778  
 KEYWORDS GSS.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 864)  
 Zabarovsky,E.R., Gizatullin,R., Podowski,R.M., Zabarovska,V.V., Xie  
 L., Muravenko,O.V., Kozlyrev,S., Petrenko,L., Skobeleva,N., Li,J.,  
 Protopopov,A., Kashuba,V., Ernberg,I., Winberg,G. and Wahlestedt,C.  
 NotI clones in the analysis of the human genome  
 Nucleic Acids Res. 28 (7), 1635-1639 (2000)  
 20175728  
 COMMENT Contact: Podowski RM  
 Center for Genomics Research  
 Karolinska Institute  
 17177 Stockholm, Sweden  
 Tel: +46-8-728-6372  
 Fax: +46-8-337983  
 Email: Raf.Podowski@cgr.ki.se  
 Class: NotI site.  
 Location/Qualifiers  
 1..864  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Human NotI clones"  
 /note="Organ: Lung; DNA was isolated from A549 cells after  
 sodium arsenite exposure for 4 weeks. This fragment was  
 differentially methylated relative to untreated controls  
 and was identified using methylation sensitive AP-PCR and  
 sequenced."

BASE COUNT 205 a 209 c 203 g 215 t 32 others  
 ORIGIN

Query Match 47.0%; Score 70; DB 17; Length 864;  
 Best Local Similarity 88.4%; Pred. No. 4.2e-13;  
 Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 49 AGTGATCCCCCGGCTGCAGAAATGCATCAAGCTTATCGATACCGTCGACCTCGAG 108  
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 DB 151 AGTGATCCCCCGGCTGCAGAAATGCATCAAGCTTATCGATACCGTCGACCTCGAG 92  
 |||||

QY 109 GGGGGGCTTAACCTAATTTTGT 134  
 |||||  
 DB 91 GGGGGGCTTAACCTAATTTTGT 66  
 |||||

RESULT 13  
 LOCUS BI306167/c 175 bp mRNA linear EST 20-JUL-2001  
 DEFINITION NL\_3\_J08 Drought stress (leaf) Oryza sativa cDNA clone NL\_3\_J08 3',  
 mRNA sequence.  
 ACCESSION BI306167  
 VERSION BI306167.1 GI:14981489  
 KEYWORDS EST.

SOURCE  
 ORGANISM  
 Oryza sativa.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 175)  
 Reddy,A.R., Ramakrishna,W., Chandrasekhar,A., Nagabhushan,I.,  
 Ravindrababu,P., and Benetzen,J.L.  
 Novel EST enrichment with normalized cDNA libraries from drought  
 stressed rice (Oryza sativa L.cv Nagina 22)  
 Unpublished (2001)  
 CONTACT Reddy AR  
 Department of Plant Sciences, School of Life Sciences  
 University of Hyderabad  
 P.O. Central University, Hyderabad-500 046, A.P, India  
 Tel: 0091-40-3010265  
 Fax: 0091-40-3010145  
 Email: arjuls@uchd.ernet.in  
 Insert Length: 175 Std Error: 0.00  
 Plate: 3 row: 7 column: 08  
 Seq primer: GPAAACGACGCGCGATC.  
 Location/Qualifiers  
 1..175  
 /organism="Oryza sativa"  
 /cultivar="Nagina 22 (indica sub sp)"  
 /db\_xref="taxon:4530"  
 /clone\_lib="NL\_3\_J08"  
 /clone\_lib="Drought stress (leaf)"  
 /tissue\_type="entire leaf tissue"  
 /dev\_stage="35 day-old seedlings"  
 /note="Organ: Leaf; Vector: T773Pac; ESTs from normalized  
 leaf cDNA library from drought stressed seedlings"

BASE COUNT 32 a 47 c 50 g 46 t  
 ORIGIN

Query Match 46.8%; Score 69.8; DB 13; Length 175;  
 Best Local Similarity 91.4%; Pred. No. 4.2e-13;  
 Matches 74; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 49 AGTGATCCCCCGGCTGCAGAAATGCATCAAGCTTATCGATACCGTCGACCTCGAG 108  
 |||||  
 DB 101 AGTGATCCCCCGGCTGCAGAAATGCATCAAGCTTATCGATACCGTCGACCTCGAG 42  
 |||||

QY 109 GGGGGGCTTAACCTAATTT 129  
 |||||  
 DB 41 GGGGGGCTTAACCTAATTT 21  
 |||||

RESULT 14  
 LOCUS BI306149/c 182 bp mRNA linear EST 20-JUL-2001  
 DEFINITION NL\_3\_I07 Drought stress (leaf) Oryza sativa cDNA clone NL\_3\_I07 3',  
 mRNA sequence.  
 ACCESSION BI306149  
 VERSION BI306149.1 GI:14981471  
 KEYWORDS EST.  
 SOURCE Oryza sativa.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 182)  
 Reddy,A.R., Ramakrishna,W., Chandrasekhar,A., Nagabhushan,I.,  
 Ravindrababu,P., and Benetzen,J.L.  
 Novel EST enrichment with normalized cDNA libraries from drought  
 stressed rice (Oryza sativa L.cv Nagina 22)  
 Unpublished (2001)  
 CONTACT Reddy AR  
 Department of Plant Sciences, School of Life Sciences  
 University of Hyderabad  
 P.O. Central University, Hyderabad-500 046, A.P, India  
 Tel: 0091-40-3010265  
 Fax: 0091-40-3010145  
 Email: arjuls@uchd.ernet.in  
 Insert Length: 175 Std Error: 0.00  
 Plate: 3 row: 7 column: 08  
 Seq primer: GPAAACGACGCGCGATC.

Email: arjuls@uohyd.ernet.in  
Insert Length: 182 Std Error: 0.00  
Plate: 3 row: 1 column: 07  
Seq primer: GTAAACGACGCCAGTG.  
Location/Qualifiers

## FEATURES

## source

1. 182  
/organism="Oryza sativa"  
/cultivar="Nagina 22 (indica sub sp)"  
/db\_xref="taxon:4530"  
/clone="NL\_3\_107"  
/clone\_lib="Drought stress (leaf)"  
/tissue\_type="Entire leaf tissue"  
/dev\_stage="35 day-old seedlings"  
/note="Organ: Leaf; Vector: T7T3Pac; ESTs from normalized  
leaf cDNA library from drought stressed seedlings "  
BASE COUNT 35 a 47 c 52 g 48 t  
ORIGIN

Query Match 46.8%; Score 69.8; DB 13; Length 182;  
Best Local Similarity 91.4%; Pred. No. 4.3e-13;  
Matches 74; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 49 AGTGGATCCCCGGGCTGCAGAAATTCGATATCAGCTTATCGATACCGTCGACCTCGAG 108  
|||||  
DB 108 AGTGGATCCCCGGGCTGCAGAAATTCGATATCAGCTTATCGATACCGTCGACCTCGAG 49  
|||||

QY 109 GGGGGCTTACTACTAATT 129  
|||||  
DB 48 GGGGGCTTCCGGTACCCCAATT 28

## RESULT 15

BI306159 182 bp mRNA linear EST 20-JUL-2001  
LOCUS NL\_3\_122 Drought stress (leaf) Oryza sativa cDNA clone NL\_3\_122 3',  
DEFINITION  
mRNA sequence.

ACCESSION BI306159

VERSION BI306159.1 GI:14981481

KEYWORDS EST.

SOURCE Oryza sativa.

ORGANISM

Oryza sativa.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 182)

Reddy, A.R., Ramakrishna, W., Chandrasekhar, A., Nagabhushan, I.,  
Ravindrababu, P. and Bennetzen, J.L.

Novel EST enrichment with normalized cDNA libraries from drought  
stressed rice (Oryza sativa L. cv Nagina 22)

Unpublished (2001)

COMMENT

CONTACT: Reddy AR

Department of Plant Sciences, School of Life Sciences  
University of Hyderabad

P.O. Central University, Hyderabad-500 046, A.P., India

Tel: 0091-40-3010265

Fax: 0091-40-3010145

Email: arjuls@uohyd.ernet.in

Insert Length: 182 Std Error: 0.00

Plate: 3 row: 1 column: 22

Seq primer: GTAAACGACGCCAGTG.

## FEATURES

## source

1. 182

/organism="Oryza sativa"

/cultivar="Nagina 22 (indica sub sp)"

/db\_xref="taxon:4530"

/clone="NL\_3\_122"

/clone\_lib="Drought stress (leaf)"

/tissue\_type="Entire leaf tissue"

/dev\_stage="35 day-old seedlings"

/note="Organ: Leaf; Vector: T7T3Pac; ESTs from normalized  
leaf cDNA library from drought stressed seedlings "

## BASE COUNT

36 a 47 c 52 g 46 t 1 others

## ORIGIN

Query Match 46.8%; Score 69.8; DB 13; Length 182;  
Best Local Similarity 91.4%; Pred. No. 4.3e-13;  
Matches 74; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 49 AGTGGATCCCCGGGCTGCAGAAATTCGATATCAGCTTATCGATACCGTCGACCTCGAG 108  
|||||  
DB 108 AGTGGATCCCCGGGCTGCAGAAATTCGATATCAGCTTATCGATACCGTCGACCTCGAG 49  
|||||

QY 109 GGGGGCTTACTACTAATT 129  
|||||  
DB 48 GGGGGCTTCCGGTACCCCAATT 28

Search completed: November 10, 2002, 08:33:11  
Job time : 1342 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 04:19:15 ; Search time 175.807 Seconds  
(without alignments)  
1908.619 Million cell updates/sec

Title: US-08-935-377-8  
Sequence: 1 GGCCCAAAATGAAAACTA.....TTGTTTGTGCGCCCGGCC 149

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*  
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*  
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*  
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6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*  
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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	149	100.0	149	21	AAA15237
2	149	100.0	149	22	ABA01478
3	149	100.0	149	24	AAD31780
4	138	92.6	150	21	AAA15238
5	138	92.6	150	22	ABA01479
6	138	92.6	150	24	AAD31781
7	137	91.9	148	22	AAA15236
8	137	91.9	148	22	ABA01477
9	137	91.9	148	24	AAD31779

10	131	87.9	145	21	AAA15235	Nucleotide sequenc
11	131	87.9	145	22	ABA01476	Partial p7.5/ATG0/
12	131	87.9	145	24	AAD31778	Modified p7.5/tk v
13	75.6	50.7	508	23	ABV39281	Human prostate exp
14	74	49.7	380	23	ABV36219	Human prostate exp
15	74	49.7	380	23	ABV45265	Human prostate exp
16	73.4	49.3	437	23	ABV38437	Human prostate exp
17	73.2	49.1	462	23	ABV32112	Human prostate exp
18	73	49.0	611	23	ABV42990	Human prostate exp
19	73	49.0	612	23	ABV34128	Human prostate exp
20	72.8	48.9	684	23	ABV36344	Human prostate exp
21	72.8	48.9	684	23	ABV45375	Human prostate exp
22	72.6	48.7	460	23	ABV33323	Human prostate exp
23	72.6	48.6	460	23	ABV42246	Human prostate exp
24	72.4	48.6	372	23	ABV43508	Human prostate exp
25	72.4	48.6	467	23	ABV45888	Human prostate exp
26	72.4	48.6	528	23	ABV38666	Human prostate exp
27	72.2	48.5	638	23	ABV4137	Human prostate exp
28	71.8	48.2	475	23	ABV30533	Human prostate exp
29	71.6	48.1	475	23	ABV39505	Human prostate exp
30	71.6	48.1	333	23	ABV45519	Human prostate exp
31	71.6	48.1	392	23	ABV38605	Human prostate exp
32	71.6	48.1	455	23	ABV31882	Human prostate exp
33	71.6	48.1	459	23	ABV35787	Human prostate exp
34	71.6	48.1	459	23	ABV44587	Human prostate exp
35	71.6	48.1	552	23	ABV35639	Human prostate exp
36	71.6	48.1	659	23	ABV39144	Human prostate exp
37	71.6	48.1	659	23	ABV45482	Human prostate exp
38	71.6	48.1	659	23	ABV45486	Human prostate exp
39	71.4	47.9	276	23	ABV35118	Human prostate exp
40	71.4	47.9	375	23	ABV44301	Human prostate exp
41	71.4	47.9	408	23	ABV35367	Human prostate exp
42	71.4	47.9	410	23	ABV32098	Human prostate exp
43	71.4	47.9	410	23	ABV38443	Human prostate exp
44	71.4	47.9	410	23	ABV41036	Human prostate exp
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## ALIGNMENTS

RESULT 1  
AAA15237  
ID AAA15237 standard; DNA; 149 BP.  
XX  
XX AAA15237;  
XX  
XX  
XX 04-SEP-2000 (first entry)  
XX  
XX  
XX Nucleotide sequence of a fragment of the plasmid p7.5/ATG2/tk.  
XX  
XX vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;  
XX  
XX vaccine; tumour regression; cancer; infection; ss.  
XX  
XX Synthetic.  
XX  
XX WC200028016-A1.  
XX  
XX 18-MAY-2000.  
XX  
XX 10-NOV-1998; 98WO-US24029.  
XX  
XX 10-NOV-1998; 98WO-US24029.  
XX  
XX 10-NOV-1998; 98WO-US24029.  
XX  
XX (VYRP ) UNIV ROCHESTER.  
XX  
XX Zauderer M;  
XX  
XX WPI: 2000-376533/32.  
XX  
XX Novel method of identifying target epitopes or antigens specific for  
XX human tumors, cancers and infected cells involving screening expression  
XX library products of a cell expressing the target epitope

```
XX PS Disclosure; Fig 2; 132pp; English.
XX CC
XX CC The present sequence represents a fragment of a vaccinia transfer
XX CC plasmid, which is used in the course of the invention. The
XX CC specification describes a method for identifying a target epitope.
XX CC The method comprises screening the products of an expression library
XX CC from a cell expressing the target epitope with cytotoxic T cells
XX CC generated against the cell to identify DNA clones expressing the target
XX CC epitope. The method may also comprise providing a cytotoxic T cell
XX CC specific for a gene product differentially expressed by a cell and
XX CC measuring the cross-reactivity of the cytotoxic T cell. The methods are
XX CC useful for identifying tumour specific target epitopes and antigens which
XX CC are useful in immunogenic compositions or vaccines to induce the
XX CC regression of tumours, cancers or infections in mammals. The genes
XX CC expressed in a panel of tumour cells that are derived from single
XX CC immortalised, non-tumorigenic cell line are used to generate HLA
XX CC restricted cytotoxic T cells which are evaluated for activity against
XX CC tumour cells. The method is useful to identify potential antigens
XX CC expressed not only by the pathogen but also by the host cells whose gene
XX CC expression is altered as a result of infection. The differential gene
XX CC expression strategies can be applied to identify immunogenic molecules
XX CC of cells infected with virus, fungus or mycobacterium.
XX SQ Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;
Query Match 100.0%; Score 149; DB 21; Length 149;
Best Local Similarity 100.0%; Pred. No. 1,7e-41;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCAAAAATTGAAAACTAGATCTATTATTGACGCGCGCGCCATGAGTGATCCCC 60
DB 1 GGGCAAAAATTGAAAACTAGATCTATTATTGACGCGCGCGCCATGAGTGATCCCC 60
QY 61 GGGCTGACGAGAAATTCATCAAGCTTATGATACCGTCGACGCGGCGGCTTAAC 120
DB 61 GGGCTGACGAGAAATTCATCAAGCTTATGATACCGTCGACGCGGCGGCTTAAC 120
QY 121 TAACATAATTTGTTTGTGGCGCGGCC 149
DB 121 TAACATAATTTGTTTGTGGCGCGGCC 149
RESULT 2
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ID ABA01478 standard; DNA; 149 BP.
XX
XX ABA01478;
XX AC
XX 04-FEB-2002 (first entry)
XX DT
XX DE Partial p7.5/ATG2/Ck sequence.
XX DE
XX DE
XX KW Cell death; toxic gene; tumour suppressor; ds.
XX OS
XX OS Synthetic.
XX OS
XX PN WO200172995-A2.
XX PD
XX PD 04-OCT-2001.
XX PF
XX PF 28-MAR-2001; 2001WO-US09953.
XX PR
XX PR 28-MAR-2000; 2000US-0192586.
XX PR 10-MAY-2000; 2000US-0203343.
XX PR 23-JAN-2001; 2001US-0263226.
XX PR 27-FEB-2001; 2001US-0271426.
XX PA
XX PA (UVRP ) UNIV ROCHESTER.
XX PI
XX PI Zauderer M, Smith ES;
XX DR
XX DR WPI; 2001.570897/64.
```

```
XX PT Selecting target polynucleotides, particularly toxic genes, involves
XX PT introducing a library of insert polynucleotides into a host cell
XX PT population, where the target polynucleotide promotes cell death -
XX PS Disclosure; Fig 8; 359pp; English.
XX CC
XX CC The present invention relates to a method for selecting a target
XX CC polynucleotide. The method comprises introducing into a host cell
XX CC population a library of insert polynucleotides, where expression of the
XX CC target polynucleotide directly or indirectly promotes host cell death.
XX CC The cells are cultured and the insert polynucleotides are collected from
XX CC the cells which die. The method is useful for selecting target
XX CC polynucleotides, particularly polynucleotides which alter cell phenotypes
XX CC of induce or inhibit cell death. The method can be used to isolate toxic
XX CC genes such as tumour suppressors. The present sequence was used to
XX CC illustrate the method of the the present invention.
XX SQ Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;
Query Match 100.0%; Score 149; DB 22; Length 149;
Best Local Similarity 100.0%; Pred. No. 1,7e-41;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCAAAAATTGAAAACTAGATCTATTATTGACGCGCGCGCCATGAGTGATCCCC 60
DB 1 GGGCAAAAATTGAAAACTAGATCTATTATTGACGCGCGCGCCATGAGTGATCCCC 60
QY 61 GGGCTGACGAGAAATTCATCAAGCTTATGATACCGTCGACGCGGCGGCTTAAC 120
DB 61 GGGCTGACGAGAAATTCATCAAGCTTATGATACCGTCGACGCGGCGGCTTAAC 120
QY 121 TAACATAATTTGTTTGTGGCGCGGCC 149
DB 121 TAACATAATTTGTTTGTGGCGCGGCC 149
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ID AAD31780 standard; DNA; 149 BP.
XX
XX AAD31780;
XX AC
XX 18-JUN-2002 (first entry)
XX DT
XX DE Modified p7.5/Ck vector, p7.5/ATG2/Ck.
XX DE
XX DE
XX KW Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
XX KW vaccine; immune response; cytostatic; p7.5/Ck vector; thymidine kinase;
XX KW p7.5/ATG2/Ck vector; ds.
XX OS
XX OS Vaccinia virus.
XX OS
XX OS Synthetic.
XX OS
XX FH Key
XX FH Location/Qualifiers
XX FT misc_signal 46..48
XX FT /tag= a
XX FT /note= "translation start codon"
XX FT 117..119
XX FT /tag= b
XX FT /note= "translation stop codon"
XX FT 121..123
XX FT /tag= c
XX FT /note= "translation stop codon"
XX FT 125..127
XX FT /tag= d
XX FT /note= "translation stop codon"
XX FT 133..139
XX FT /tag= e
XX FT /note= "transcription stop signal"
XX PN
XX PN US2002018765-A1.
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PD 14-FEB-2002.
XX
PF 02-APR-2001; 2001US-0822250.
XX
PR 22-SEP-1997; 97US-0935377.
XX
PA (UVRP ) UNIV ROCHESTER.
XX
PI Zauderer M;
XX
DR WPI: 2002-239252/29.
XX
PT Representational Difference Analysis method for identification of
PT antigens recognized by cytotoxic T cells and specific for human tumors,
PT comprises improved selection of genes encoding target antigens
XX
XX Example 1; Fig 2; 54pp; English.
XX
CC The present invention relates to novel methods for the identification
CC of antigens recognised by cytotoxic T cells (CTLs) and specific for
CC human tumours, cancers and infected cells. The method involves screening
CC the products of an expression library generated from DNA/RNA of a cell
CC expressing a target epitope with cytotoxic T cells generated against
CC the cell to identify DNA clones expressing target epitope or providing
CC cytotoxic T cells specific for a gene product differentially expressed
CC by a cell and measuring the cross-reactivity of the cytotoxic T cells
CC for cells expressing a target epitope in which the target epitope is
CC identified as a gene product inducing cytotoxic T cells. The method is
CC useful for identifying a target epitope or antigen specific for a tumour
CC cell. The target epitope is also useful for identifying target antigens
CC in other target cells against which it is desirable to induce cell-
CC mediated immunity. The antigen identified by the method is useful
CC in immunogenic compositions and vaccine preparations to induce the
CC regression of tumours, cancers and infections in mammals. The invention
CC also relates to vaccinia viral vectors which are useful for treating
CC tumour-bearing mammals, including humans to generate immune response
CC against the tumour cells. They are also useful for immunising or
CC vaccinating tumour-free subjects to prevent tumour formation. The
CC present sequence is modified p7.5/tk (thymidine kinase) vector,
CC p7.5/ATG2/tk. This vector comprises a vaccinia virus 7.5K promoter and
CC a modified tk DNA fragment. This vector is used in the exemplification
CC of the invention.
XX
SQ Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;
XX
Query Match 100.0%; Score 149; DB 24; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.7e-41;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GGCCAAAATGAAAACCTGATCTATTATTGACGCGCGCCGCGCATGATGATCCCC 60
DB 1 GGCCAAAATGAAAACCTGATCTATTATTGACGCGCGCGCCGCGCATGATGATCCCC 60
XX
QY 61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATCGTCGACGCGGGGGGCGCTTAAC 120
DB 61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATCGTCGACGCGGGGGGCGCTTAAC 120
XX
QY 121 TAACTAATTTTGTGTTTGTGGGCGCGCC 149
DB 121 TAACTAATTTTGTGTTTGTGGGCGCGCC 149
XX
RESULT 4
AAAI5238
ID AAAI5238 standard; DNA; 150 BP.
XX
AC AAAI5238;
XX
DT 04-SEP-2000 (first entry)
XX
DE Nucleotide sequence of a fragment of the plasmid p7.5/ATG3/tk.
XX
KM Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;
```

```
KW vaccine; tumour regression; cancer; infection; ss.
XX
XX Synthetic.
XX
XX WO200028016-A1.
XX
XX 18-MAY-2000.
XX
XX 10-NOV-1998; 98WO-US24029.
XX
XX 10-NOV-1998; 98WO-US24029.
XX
XX (UVRP ) UNIV ROCHESTER.
XX
XX Zauderer M;
XX
XX WPI: 2000-376533/32.
XX
XX
XX Novel method of identifying target epitopes or antigens specific for
XX human tumors, cancers and infected cells involving screening expression
XX library products of a cell expressing the target epitope
XX
XX Disclosure; Fig 2; 132pp; English.
XX
CC The present sequence represents a fragment of a vaccinia transfer
CC plasmid, which is used in the course of the invention. The
CC specification describes a method for identifying a target epitope.
CC The method comprises screening the products of an expression library
CC from a cell expressing the target epitope with cytotoxic T cells
CC generated against the cell to identify DNA clones expressing the target
CC epitope. The method may also comprise providing a cytotoxic T cell
CC specific for a gene product differentially expressed by a cell and
CC measuring the cross-reactivity of the cytotoxic T cell. The methods are
CC useful for identifying tumour specific target epitopes and antigens which
CC are useful in immunogenic compositions or vaccines to induce the
CC regression of tumors, cancers or infections in mammals. The genes
CC expressed in a panel of tumour cells that are derived from single
CC immortalised, non-tumorigenic cell line are used to generate RNA
CC restricted cytotoxic T cells which are evaluated for activity against
CC tumour cells. The method is useful to identify potential antigens
CC expressed not only by the pathogen but also by the host cells whose gene
CC expression is altered as a result of infection. The differential gene
CC expression strategies can be applied to identify immunogenic molecules
CC of cells infected with virus, fungus or mycobacterium.
XX
SQ Sequence 150 BP; 36 A; 38 C; 39 G; 37 T; 0 other;
XX
Query Match 92.6%; Score 138; DB 21; Length 150;
Best Local Similarity 99.3%; Pred. No. 1.1e-37;
Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX
QY 1 GGCCAAAATGAAAACCTGATCTATTATTGACGCGCGCGCCATGA-GTGGATCCCC 59
DB 1 GGCCAAAATGAAAACCTGATCTATTATTGACGCGCGCGCCATGACGTGATCCCC 60
XX
QY 60 CGGCTGCAGGAATTCGATATCAAGCTTATCGATCGTCGACGCGGGGGGCGCTTAA 119
DB 61 CGGCTGCAGGAATTCGATATCAAGCTTATCGATCGTCGACGCGGGGGGCGCTTAA 120
XX
QY 120 CTACTAATTTTGTGTTTGTGGGCGCGCC 149
DB 121 CTACTAATTTTGTGTTTGTGGGCGCGCC 150
XX
RESULT 5
ABAO1479
ID ABAO1479 standard; DNA; 150 BP.
XX
AC ABAO1479;
XX
DT 04-FEB-2002 (first entry)
XX
DE Partial p7.5/ATG3/tk sequence.
```

XX Cell death; toxic gene; tumour suppressor; ds.  
KM Synthetic.  
XX WO200172995-A2.  
PN 04-OCT-2001.  
XX 28-MAR-2001; 2001WO-US09953.  
PF 28-MAR-2000; 2000US-0192586.  
XX 10-MAY-2000; 2000US-0203343.  
PR 23-JAN-2001; 2001US-0263226.  
PR 27-FEB-2001; 2001US-0271426.  
XX (UYRP ) UNIV ROCHESTER.  
XX Zauderer M, Smith ES;  
PI WPI; 2001-570897/64.  
DR  
XX  
XX Selecting target polynucleotides, particularly toxic genes, involves  
PT introducing a library of insert polynucleotides into a host cell  
PT producing a library of insert polynucleotide promotes cell death -  
XX  
XX Disclosure; Fig 8; 359pp; English.  
XX  
XX The present invention relates to a method for selecting a target  
CC polynucleotide. The method comprises introducing into a host cell  
CC a population a library of insert polynucleotides, where expression of the  
CC target polynucleotide directly or indirectly promotes host cell death.  
CC The cells are cultured and the insert polynucleotides are collected from  
CC the cells which die. The method is useful for selecting target  
CC polynucleotides, particularly polynucleotides which alter cell phenotypes  
CC of induce or inhibit cell death. The method can be used to isolate toxic  
CC genes such as tumour suppressors. The present sequence was used to  
CC illustrate the method of the present invention.  
XX  
XX Sequence 150 BP; 36 A; 38 C; 39 G; 37 T; 0 other;  
SQ  
Query Match 92.6%; Score 138; DB 22; Length 150;  
Best Local Similarity 99.3%; Pred. No. 1.1e-37;  
Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 GGCCAAAATTGAAAACAGATCTATTATTCGACGCGCGCCCATGA-GTGGATCCCC 59  
Db 1 GGCCAAAATTGAAAACAGATCTATTATTCGACGCGCGCCCATGA-GTGGATCCCC 60  
QY 60 CGGCTGTCAGGAATTCGATATCAAGCTTATCGATACCGTGCAGCTCGAGGGGGGCTTAA 119  
Db 61 CGGCTGTCAGGAATTCGATATCAAGCTTATCGATACCGTGCAGCTCGAGGGGGGCTTAA 120  
QY 120 CTAACTAATTTTGTGTTTGTGGCGCCGCC 149  
Db 121 CTAACTAATTTTGTGTTTGTGGCGCCGCC 150  
RESULT 6  
AAD31781  
ID AAD31781 standard; DNA: 150 BP.  
XX AAD31781;  
AC  
XX 18-JUN-2002 (first entry)  
DT  
XX Modified p7.5/tk vector, p7.5/ATG3/tk.  
DE  
XX Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;  
KM vaccine; immune response; cytostatic; p7.5/tk vector; thymidine kinase;  
KM p7.5/ATG3/tk vector; ds.  
XX  
XX Vaccinia virus.

OS Synthetic.  
XX Location/Qualifiers  
FH Key 46..48  
FT misc\_signal /tag= a  
FT /note= "Translation start codon"  
FT 118..120  
FT /tag= b  
FT /note= "Translation stop codon"  
FT 122..124  
FT misc\_signal /tag= c  
FT /note= "Translation stop codon"  
FT 126..128  
FT misc\_signal /tag= d  
FT /note= "Translation stop codon"  
FT 134..140  
FT misc\_signal /tag= e  
FT /note= "Transcription stop signal"  
XX  
XX US2002018785-A1.  
XX  
XX 14-FEB-2002.  
XX  
XX 02-APR-2001; 2001US-0822250.  
XX  
XX 22-SEP-1997; 97US-0935377.  
XX  
XX (UYRP ) UNIV ROCHESTER.  
XX  
XX Zauderer M;  
PI WPI; 2002-239252/29.  
DR  
XX  
XX Representational Difference Analysis method for identification of  
PT antigens recognised by cytotoxic T cells and specific for human tumors,  
PT comprises improved selection of genes encoding target antigens -  
XX  
XX Example 1; Fig 2; 54pp; English.  
XX  
XX The present invention relates to novel methods for the identification  
CC of antigens recognised by cytotoxic T cells (CTLs) and specific for  
CC human tumors, cancers and infected cells. The method involves screening  
CC the products of an expression library generated from DNA/RNA of a cell  
CC expressing a target epitope with cytotoxic T cells generated against  
CC the cell to identify DNA clones expressing target epitope or providing  
CC cytotoxic T cells specific for a gene product differentially expressed  
CC by a cell and measuring the cross-reactivity of the cytotoxic T cells  
CC for cells expressing a target epitope in which the target epitope is  
CC identified as a gene product inducing cytotoxic T cells. The method is  
CC useful for identifying a target epitope or antigen specific for a tumour  
CC cell. The target epitope is also useful for identifying target antigens  
CC in other target cells against which it is desirable to induce cell-  
CC mediated immunity. The antigen identified by the method is useful  
CC in immunogenic compositions and vaccine preparations to induce the  
CC regression of tumours, cancers and infections in mammals. The invention  
CC also relates to vaccinia viral vectors which are useful for treating  
CC tumour-bearing mammals, including humans to generate immune response  
CC against the tumour cells. They are also useful for immunising or  
CC vaccinating tumour-free subjects to prevent tumour formation. The  
CC present sequence is modified p7.5/tk (thymidine kinase) vector,  
CC p7.5/ATG3/tk. This vector comprises a vaccinia virus 7.5k promoter and  
CC a modified tk DNA fragment. This vector is used in the exemplification  
CC of the invention.  
XX  
XX Sequence 150 BP; 36 A; 38 C; 39 G; 37 T; 0 other;  
SQ  
Query Match 92.6%; Score 138; DB 24; Length 150;  
Best Local Similarity 99.3%; Pred. No. 1.1e-37;  
Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 GGCCAAAATTGAAAACAGATCTATTATTCGACGCGCGCCCATGA-GTGGATCCCC 59  
Db 1 GGCCAAAATTGAAAACAGATCTATTATTCGACGCGCGCCCATGA-GTGGATCCCC 60



OY 60 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCGTCGAGGGGGCCCTAA 119  
|||||  
DB 61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCGTCGAGGGGGCCCTAA 120  
OY 120 CTAATTAATTTGTTTGTGTGGCCCGGCC 149  
|||||  
DB 121 CTAATTAATTTGTTTGTGTGGCCCGGCC 150

## RESULT 7

AAAI5236

ID AAAI5236 standard; DNA; 148 BP.

AC AAAI5236;

DT 04-SEP-2000 (first entry)

DE Nucleotide sequence of a fragment of the plasmid p7.5/ATG1/tk.

KW Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;  
KM vaccine; tumour regression; cancer; infection; ss.

XX Synthetic.

PN WO200028016-A1.

PD 18-MAY-2000.

PF 10-NOV-1998; 98MO-US24029.

PR 10-NOV-1998; 98MO-US24029.

PA (UVRP ) UNIV ROCHESTER.

PI Zauderer M;

DR WPI; 2000-376533/32.

XX Novel method of identifying target epitopes or antigens specific for  
PT human tumors, cancers and infected cells involving screening expression  
PT library products of a cell expressing the target epitope -

XX Disclosure; Fig 2; 132pp; English.

XX PS

CC The present sequence represents a fragment of a vaccinia transfer  
CC plasmid, which is used in the course of the invention. The  
CC specification describes a method for identifying a target epitope.CC The method comprises screening the products of an expression library  
CC from a cell expressing the target epitope with cytotoxic T cells  
CC generated against the cell to identify DNA clones expressing the target  
CC epitope. The method may also comprise providing a cytotoxic T cell  
CC specific for a gene product differentially expressed by a cell and  
CC measuring the cross-reactivity of the cytotoxic T cell. The methods are  
CC useful for identifying tumour specific target epitopes and antigens which  
CC are useful in immunogenic compositions or vaccines to induce the  
CC regression of tumors, cancers or infections in mammals. The genes  
CC expressed in a panel of tumour cells that are derived from single  
CC immunotised, non-tumorigenic cell line are used to generate HLA  
CC restricted cytotoxic T cells which are evaluated for activity against  
CC tumour cells. The method is useful to identify potential antigens  
CC expressed not only by the pathogen but also by the host cells whose gene  
CC expression is altered as a result of infection. The differential gene  
CC expression strategies can be applied to identify immunogenic molecules  
CC of cells infected with virus, fungus or mycobacterium.

CC XX

CC XX

CC XX

CC XX

CC XX

CC XX

CC XX

CC XX

CC XX

CC XX

CC XX

CC XX

SQ Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;

Query Match

Best Local Similarity 91.9%; Score 137; DB 22; Length 148;

Matches 148; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 GGCCAAAATTAAGAACTAGATCTATTATTGCAAGCGGCCGCGCATGATGATCCCC 60

DB 1 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCGTCGAGGGGGCCCTAAC 59  
|||||

OY 61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCGTCGAGGGGGCCCTAAC 120  
|||||

DB 60 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCGTCGAGGGGGCCCTAAC 119  
|||||

OY 121 TAACATAATTTGTTTGTGTGGCCCGGCC 149  
|||||

DB 120 TAACATAATTTGTTTGTGTGGCCCGGCC 148

## RESULT 8

ABA01477

ID ABA01477 standard; DNA; 148 BP.

AC ABA01477;

DT 04-FEB-2002 (first entry)

DE Partial p7.5/ATG1/tk sequence.

KW Cell death; toxic gene; tumour suppressor; ds.

XX Synthetic.

PN WO200172995-A2.

PD 04-OCT-2001.

PF 28-MAR-2001; 2001WO-US09953.

PR 28-MAR-2000; 2000US-0192586.

PR 10-MAY-2000; 2000US-0203343.

PR 23-JAN-2001; 2001US-0263226.

PR 27-FEB-2001; 2001US-0271426.

PA (UVRP ) UNIV ROCHESTER.

PI Zauderer M, Smith ES;

DR WPI; 2001-570897/64.

XX Selecting target polynucleotides, particularly toxic genes, involves  
PT introducing a library of insert polynucleotides into a host cell  
PT population, where the target polynucleotide promotes cell death -

XX PS Disclosure; Fig 8; 359pp; English.

CC The present invention relates to a method for selecting a target  
CC polynucleotide. The method comprises introducing into a host cell  
CC population a library of insert polynucleotides, where expression of the  
CC target polynucleotide directly or indirectly promotes host cell death.CC The cells are cultured and the insert polynucleotides are collected from  
CC the cells which die. The method is useful for selecting target  
CC polynucleotides, particularly polynucleotides which alter cell phenotypes  
CC of induce or inhibit cell death. The method can be used to isolate toxic  
CC genes such as tumour suppressors. The present sequence was used to  
CC illustrate the method of the the present invention.

CC XX

CC XX

CC XX

CC XX

CC XX

CC XX

CC XX

CC XX

CC XX

SQ Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;

Query Match

Best Local Similarity 91.9%; Score 137; DB 22; Length 148;

Matches 148; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 GGCCAAAATTAAGAACTAGATCTATTATTGCAAGCGGCCGCGCATGATGATCCCC 60  
|||||DB 1 GGCCAAAATTAAGAACTAGATCTATTATTGCAAGCGGCCGCGCATGATGATCCCC 59  
|||||OY 61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCGTCGAGGGGGCCCTAAC 120  
|||||DB 60 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCGTCGAGGGGGCCCTAAC 119  
|||||

Oy	121	TACTAATTTGTTTTGTGGGCCCGCCG	149
Db	120	TAACTAAATTGTGTTTGtggcccgccc	148
<hr/>			
RESULT 9			
ID	AAD31779	standard; DNA: 148 BP.	
XX	AC	AAD31779:	
XX	DT	18-JUN-2002 (first entry)	
XX	DE	Modified p7.5/tk vector, p7.5/WTG1/tk.	
XX	KM	Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;	
XX	KW	vaccine; immune response; cytostatic; p7.5/tk vector; thymidine kinase;	
OS	OS	p7.5/WTG1/tk vector; ds.	
XX	XX	Vaccinia virus.	
XX	XX	Synthetic.	
PH	FT	Key	Location/Qualifiers
FT	FT	misc_signal	46..48
FT	FT	/tag= a	
FT	FT	/note= "translation start codon"	
FT	FT	misc_signal	116..118
FT	FT	/tag= b	
FT	FT	/note= "translation stop codon"	
FT	FT	misc_signal	120..122
FT	FT	/tag= c	
FT	FT	/note= "translation stop codon"	
FT	FT	misc_signal	124..126
FT	FT	/tag= d	
FT	FT	/note= "translation stop codon"	
FT	FT	misc_signal	132..138
FT	FT	/tag= e	
FT	FT	/note= "transcription stop signal"	
PX	PX	US2002018785-A1.	
PD	PD	14-FEB-2002.	
PX	PX	02-APR-2001; 2001US-0822250.	
PF	PF	22-SEP-1997; 97US-0935377.	
PX	PX	(UYRP ) UNIV ROCHESTER.	
PA	PI	Zauderer M;	
PX	PX	WPL; 2002-239252/29.	
DR	DR	Representational Difference Analysis method for identification of	
PX	PX	antigens recognized by cytotoxic T cells and specific for human tumors,	
PT	PT	comprises improved selection of genes encoding target antigens	
PS	PS	Example 1; Fig 2; 54pp; English.	
XX	XX	The present invention relates to novel methods for the identification	
CC	CC	of antigens recognised by cytotoxic T cells (CTLs) and specific for	
CC	CC	human tumours, cancers and infected cells. The method involves screening	
CC	CC	the products of an expression library generated from DNA/RNA of a cell	
CC	CC	expressing a target epitope with cytotoxic T cells generated against	
CC	CC	the cell to identify DNA clones expressing target epitope or providing	
CC	CC	cytotoxic T cells specific for a gene product differentially expressed	
CC	CC	by a cell and measuring the cross-reactivity of the cytotoxic T cells	
CC	CC	for cells expressing a target epitope in which the target epitope is	
CC	CC	identified as a gene product inducing cytotoxic T cells. The method is	
CC	CC	useful for identifying a target epitope or antigen specific for a tumour	
CC	CC	cell. The target epitope is also useful for identifying target antigens	
CC	CC	in other target cells against which it is desirable to induce cell-	

Query Match	91.9%	Score 137	DB 24	Length 148
Best Local Similarity	99.3%	Pred. NO. 2.3e-37		
Matches 148	Conservative %	0	Mismatches	1
			Indels	Gaps
CC mediated immunity. The antigen identified by the method is useful				
CC in immunogenic compositions and vaccine preparations to induce the				
CC regression of tumours, cancers and infections in mammals. The invention				
CC also relates to vaccinia viral vectors which are useful for treating				
CC tumour-bearing mammals, including humans to generate immune response				
CC against the tumour cells. They are also useful for immunising or				
CC vaccinating tumour-free subjects to prevent tumour formation. The				
CC present sequence is modified p7.5/tk (thymidine kinase) vector. The				
CC p7.5/ANG1/tk. This vector comprises a vaccinia virus 7.5k promoter and				
CC a modified tk DNA fragment. This vector is used in the exemplification				
CC of the invention.				
CC				
XX Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;				
XX				
YY Query Match	91.9%	Score 137	DB 24	Length 148
YY Best Local Similarity	99.3%	Pred. NO. 2.3e-37		
YY Matches 148	Conservative %	0	Mismatches	1
YY			Indels	Gaps
DB 1	GGCCAAAATTGAAAACTAGATCTATTATTTGACGGCGGCATGATGATCCGCC	60		
DB 1	GGCCAAAATTGAAAACTAGATCTATTATTTGACGGCGGCATG-GTGATTCGCC	59		
QY 61	GGGCGACGAGTAATTCGATATCAAGCTATTCGATCCGTCGACCTCGAGGGGGCCTAAC	120		
DB 60	GGGCTGTCAGGAATTCGATATCAAGCTATTCGATACCGTCGACCTCGAGGGGGCCTAAC	119		
QY 121	TAACTAATTTTGTGTTTGTGGCCCGGCC	149		
DB 120	TAACTAATTTTGTGTTTGTGGCCCGGCC	148		
RESULT 10				
AAAI5235				
ID AAAI5235	standard; DNA; 145 BP.			
XX				
AC AAAI5235;				
XX				
DT 04-SEP-2000	(first entry)			
XX				
DE Nucleotide sequence of a fragment of the plasmid p7.5/ANG0/tk.				
XX				
KM Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;				
KW vaccine; tumour regression; cancer; infection; ss.				
XX				
OS Synthetic.				
XX				
PN MO200028016-A1.				
XX				
PD 18-MAY-2000.				
PF 10-NOV-1998;	98WO-US24029.			
XX				
PR 10-NOV-1998;	98WO-US24029.			
XX				
PA (UYRP ) UNIV ROCHESTER.				
XX				
PI Zauderer M;				
XX				
DR WPI; 2000-376533/32.				
XX				
PT Novel method of identifying target epitopes or antigens specific for				
PT human tumors, cancers and infected cells involving screening expression				
PT library products of a cell expressing the target epitope -				
XX				
PS Disclosure; Fig 2; 132pp; English.				
XX				
CC The present sequence represents a fragment of a vaccinia transfer				
CC plasmid, which is used in the course of the invention. The				
CC specification describes a method for identifying a target epitope.				
CC The method comprises screening the products of an expression library				
CC from a cell expressing the target epitope with cytotoxic T cells				
CC generated against the cell to identify DNA clones expressing the target				
CC epitope. The method may also comprise providing a cytotoxic T cell				

CC specific for a gene product differentially expressed by a cell and  
 CC measuring the cross-reactivity of the cytotoxic T cell. The methods are  
 CC useful for identifying tumor specific target epitopes and antigens which  
 CC are useful in immunogenic compositions or vaccines to induce the  
 CC regression of tumors, cancers or infections in mammals. The genes  
 CC expressed in a panel of tumor cells that are derived from single  
 CC immortalised, non-tumorigenic cell line are used to generate HLA  
 CC restricted cytotoxic T cells which are evaluated for activity against  
 CC tumor cells. The method is useful to identify potential antigens  
 CC expressed not only by the pathogen but also by the host cells whose gene  
 CC expression is altered as a result of infection. The differential gene  
 CC expression strategies can be applied to identify immunogenic molecules  
 CC of cells infected with virus, fungus or mycobacterium.

SO Sequence 145 BP; 34 A; 37 C; 38 G; 36 T; 0 other;

Query Match 87.9%; Score 131; DB 21; Length 145;  
 Best Local Similarity 97.3%; Pred. No. 2.7e-35;  
 Matches 145; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 GGGCAAAATTTGAAACTAGATCTATTATTGACAGCGCGCCCATGATGATCCCC 60  
 DB 1 GGGCAAAATTTGAAACTAGATCTATTATTGACAGCGCGCCCATGATGATCCCC 56  
 QY 61 GGGCTGCAGGAATTCGATATCAAGCTTATGATACCGTCGACCTCGAGGGGGGCTTAC 120  
 DB 57 GGGCTGCAGGAATTCGATATCAAGCTTATGATACCGTCGACCTCGAGGGGGGCTTAC 116  
 QY 121 TAACATAATTTGTTTTGTGGGCCCGGCC 149  
 DB 117 TAACATAATTTGTTTTGTGGGCCCGGCC 145

## RESULT 11

ABA01476  
 ID ABA01476 standard; DNA; 145 BP.

XX ABA01476;

AC 04-FEB-2002 (first entry)

DT Partial p7.5/ATG0/tk sequence.

DE Cell death; toxic gene; tumour suppressor; ds.

KW Synthetic.

OS WO200172995-A2.

PN 04-OCT-2001.

PD 28-MAR-2001; 2001NO-US09953.

PF 28-MAR-2001; 2000US-0192586.

PR 10-MAY-2000; 2000US-0203343.

PR 23-JAN-2001; 2001US-0263226.

PR 27-FEB-2001; 2001US-0271426.

PA (UTRP ) UNIV ROCHESTER.

PI Zauderer M, Smith ES;

PD WPI; 2001-570897/64.

PT Selecting target polynucleotides, particularly toxic genes, involves  
 PT introducing a library of insert polynucleotides into a host cell  
 PT population, where the target polynucleotide promotes cell death -  
 PS Disclosure; Fig 8; 359pp; English.

CC The present invention relates to a method for selecting a target  
 CC polynucleotide. The method comprises introducing into a host cell  
 CC population a library of insert polynucleotides, where expression of the

CC target polynucleotide directly or indirectly promotes host cell death.  
 CC The cells are cultured and the insert polynucleotides are collected from  
 CC the cells which die. The method is useful for selecting target  
 CC polynucleotides, particularly polynucleotides which alter cell phenotypes  
 CC of induce or inhibit cell death. The method can be used to isolate toxic  
 CC genes such as tumour suppressors. The present sequence was used to  
 CC illustrate the method of the the present invention.

SO Sequence 145 BP; 34 A; 37 C; 38 G; 36 T; 0 other;

Query Match 87.9%; Score 131; DB 22; Length 145;  
 Best Local Similarity 97.3%; Pred. No. 2.7e-35;  
 Matches 145; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 GGGCAAAATTTGAAACTAGATCTATTATTGACAGCGCGCCCATGATGATCCCC 60  
 DB 1 GGGCAAAATTTGAAACTAGATCTATTATTGACAGCGCGCCCATGATGATCCCC 56  
 QY 61 GGGCTGCAGGAATTCGATATCAAGCTTATGATACCGTCGACCTCGAGGGGGGCTTAC 120  
 DB 57 GGGCTGCAGGAATTCGATATCAAGCTTATGATACCGTCGACCTCGAGGGGGGCTTAC 116  
 QY 121 TAACATAATTTGTTTTGTGGGCCCGGCC 149  
 DB 117 TAACATAATTTGTTTTGTGGGCCCGGCC 145

## RESULT 12

AAD31778  
 ID AAD31778 standard; DNA; 145 BP.

XX AAD31778;

DT 18-JUN-2002 (first entry)

DE Modified p7.5/tk vector, p7.5/ATG0/tk.

KW Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;

KW vaccine; immune response; cytostatic; p7.5/tk vector; thymidine kinase;

KW p7.5/ATG0/tk vector; ds.

OS Vaccinia virus.

OS Synthetic.

XX Key

FT misc\_signal

FT misc\_signal

FT misc\_signal

FT misc\_signal

FT misc\_signal

FT misc\_signal

FT misc\_signal

FT misc\_signal

FT misc\_signal

FT misc\_signal

FT misc\_signal

FT misc\_signal

FT misc\_signal

FT misc\_signal

FT misc\_signal

US2002018785-A1.

14-FEB-2002.

02-APR-2001; 2001US-0822250.

22-SEP-1997; 97US-0935377.

(UTRP ) UNIV ROCHESTER.

Zauderer M;

WPI; 2002-239252/29.

Representational Difference Analysis method for identification of



```
PR 13-DEC-2000; 2000US-255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA Schlegel R, Endege WO, Monahan JE;
XX WPI: 2001-662795/76.
DR
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 7497; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 380 BP; 106 A; 89 C; 93 G; 92 T; 0 other;

Query Match 49.7%; Score 74; DB 23; Length 380;
Best Local Similarity 73.1%; Pred. No. 1.5e-15;
Matches 95; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

OY 5 AAAAAATGAAACTAGATCTATTATTGCAAGCGCGCCCGCATGAGTCCCGGGG 64
DB 103 ACAATTTATAGTTAATACGAAAGTTACCGCTAGAACTAGTGGATCCCCGGGG 162
OY 65 TGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTTAAC 124
DB 163 TGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCGTACC 222
OY 125 TAATTTGTT 134
DB 223 AGCTTTGTT 232

RESULT 15
ABV45265
ID ABV45265 standard; cDNA; 380 BP.
XX
AC ABV45265;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 45256.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
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PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA Schlegel R, Endege WO, Monahan JE;
XX WPI: 2001-662795/76.
DR
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 8960; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 380 BP; 106 A; 89 C; 93 G; 92 T; 0 other;

Query Match 49.7%; Score 74; DB 23; Length 380;
Best Local Similarity 73.1%; Pred. No. 1.5e-15;
Matches 95; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

OY 5 AAAAAATGAAACTAGATCTATTATTGCAAGCGCGCCCGCATGAGTCCCGGGG 64
DB 103 ACAATTTATAGTTAATACGAAAGTTACCGCTAGAACTAGTGGATCCCCGGGG 162
OY 65 TGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTTAAC 124
DB 163 TGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCGTACC 222
OY 125 TAATTTGTT 134
DB 223 AGCTTTGTT 232
```

Search completed: November 10, 2002, 05:58:28  
Job time : 175.807 secs



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## OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:58:40 ; Search time 37.0825 Seconds

(without alignments)  
1425,554 Million cell updates/sec

Title: US-08-935-377-8

149

Sequence: 1 GCCCAAAATTGAAACTA.....TTGTTTGTGGCGCCGCC 149

## Scoring table:

IDENTITY-NUC  
Gapop 10.0 , Gapext 1.0

## Searched:

320260 seqs, 177392727 residues

Total number of hits satisfying chosen parameters: 640520

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

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2: /cgn2_6/ptodata/1/pubpna/PCCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	149	100.0	149	10	US-09-822-250-8	Sequence 8, Appli
2	149	100.0	149	10	US-09-987-456-4	Sequence 4, Appli
3	138	92.6	150	10	US-09-822-250-9	Sequence 9, Appli
4	138	92.6	150	10	US-09-987-456-5	Sequence 9, Appli
5	137	91.9	148	10	US-09-822-250-7	Sequence 7, Appli
6	137	91.9	148	10	US-09-987-456-3	Sequence 3, Appli
7	131	87.9	145	10	US-09-822-250-6	Sequence 6, Appli
8	131	87.9	145	10	US-09-987-456-2	Sequence 2, Appli
9	70	47.0	424	10	US-09-834-975-601	Sequence 601, App
10	69.4	46.6	858	10	US-09-735-705-91	Sequence 91, Appl
11	69.4	46.6	858	10	US-09-850-716A-91	Sequence 91, Appl
12	69.4	46.6	858	10	US-09-897-778-91	Sequence 91, Appl
13	68.6	46.0	457	10	US-09-735-705-306	Sequence 306, App
14	68.6	46.0	457	10	US-09-850-716A-306	Sequence 306, App
15	68.6	46.0	457	10	US-09-897-778-306	Sequence 306, App
16	68	45.6	118	10	US-09-784-130-9	Sequence 306, App
17	68	45.6	752	10	US-09-956-004-108	Sequence 108, App
18	67.8	45.5	545	10	US-09-810-936-10	Sequence 10, Appl
19	67.8	45.5	545	10	US-09-429-755-10	Sequence 10, Appl

C 20	66.8	44.8	574	10	US-09-834-975-541	Sequence 541, App
C 21	64	43.0	661	10	US-09-912-447-16	Sequence 16, Appl
C 22	62	41.6	105	10	US-09-974-300-7717	Sequence 7717, Ap
C 23	61	40.9	62	10	US-09-557-423-1	Sequence 1, Appli
C 24	55.8	37.4	624	10	US-09-834-975-469	Sequence 469, App
C 25	53.4	35.8	1094	10	US-09-932-418-3	Sequence 3, Appli
C 26	51.8	34.8	4633	10	US-09-880-107-3822	Sequence 3822, Ap
C 27	50.8	34.1	343	10	US-09-924-035A-839	Sequence 839, App
C 28	49.8	33.4	1981	10	US-09-908-322-26	Sequence 26, Appl
C 29	49.8	33.4	6244	10	US-09-281-674-8	Sequence 8, Appli
C 30	49.8	33.4	6244	10	US-09-892-227-8	Sequence 8, Appli
C 31	49.6	33.3	332	10	US-09-823-114-14	Sequence 14, Appl
C 32	49.6	32.9	100	10	US-09-380-728A-19	Sequence 19, Appl
C 33	49	32.9	1329	10	US-09-925-259-240	Sequence 240, App
C 34	49	32.9	2790	10	US-09-739-254-30	Sequence 30, Appl
C 35	49	32.9	2790	10	US-09-904-615-30	Sequence 30, Appl
C 36	48.8	32.8	69	10	US-09-822-250-1	Sequence 1, Appli
C 37	48.8	32.8	69	10	US-09-987-456-140	Sequence 140, App
C 38	48.4	32.5	53	10	US-09-822-250-23	Sequence 23, Appl
C 39	48.4	32.5	57	10	US-09-822-250-5	Sequence 5, Appli
C 40	48.4	32.5	57	10	US-09-987-456-1	Sequence 1, Appli
C 41	48	32.2	57	10	US-09-955-649-4	Sequence 4, Appli
C 42	48	32.2	57	10	US-09-973-013-4	Sequence 4, Appli
C 43	48	32.2	341	10	US-09-735-705-302	Sequence 302, App
C 44	48	32.2	341	10	US-09-850-716A-302	Sequence 302, App
C 45	48	32.2	341	10	US-09-897-778-302	Sequence 302, App

## ALIGNMENTS

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RESULT 1
US-09-822-250-8
; Sequence 8, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zedeler, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 149
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-822-250-8
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Query Match 100.0%; Score 149; DB 10; Length 149;  
Best Local Similarity 100.0%; Pred. No. 1.2e+46;  
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCCCAAAATTGAAACTAGATCTATTATTCACGCGCGCCGCGATGAGTGATCCGCC 60
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Db 1 GCCCAAAATTGAAACTAGATCTATTATTCACGCGCGCGCGATGAGTGATCCGCC 60
QY 61 GGGCTCAGGAATTCATTCACAGCTTATCGATACCGTGACCTGAGGGGGGCGCTAAC 120
   |||
Db 61 GGGCTCAGGAATTCATTCACAGCTTATCGATACCGTGACCTGAGGGGGGCGCTAAC 120
QY 121 TAACATAATTTGTTTGTGGCGCGCCGCC 149
   |||
Db 121 TAACATAATTTGTTTGTGGCGCGCCGCC 149
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RESULT 2  
US-09-987-456-4  
; Sequence 4, Application US/09987456  
; Patent No. US20020123057A1  
; GENERAL INFORMATION:

APPLICANT: University of Rochester  
APPLICANT: Zauderer, Maurice  
APPLICANT: Ernest S. Smith  
TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting  
TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells  
FILE REFERENCE: 1821.0070004  
CURRENT APPLICATION NUMBER: US/09/987,456  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/271,424  
PRIOR FILING DATE: 2001-02-27  
PRIOR APPLICATION NUMBER: 60/262,067  
PRIOR FILING DATE: 2001-01-18  
PRIOR APPLICATION NUMBER: 60/298,087  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/249,268  
PRIOR FILING DATE: 2000-11-17  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 149  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: p7.5/ATG2/lk vector  
US-09-987-456-4

Query Match 100.0%; Score 149; DB 10; Length 149;  
Best Local Similarity 100.0%; Pred. No. 1.2e-46;  
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCAAAATTTGAAAATCTATTTATTTGACGCGCGCCCATGAGTGCATCCCC 60  
1 GGGCAAAATTTGAAAATCTATTTATTTGACGCGCGCCCATGAGTGCATCCCC 60  
DB 1 GGGCTGACGAATTCGATCAACGCTTATGATACCGTGCACCTCGAGGGGGGCTAAC 120  
61 GGGCTGACGAATTCGATCAACGCTTATGATACCGTGCACCTCGAGGGGGGCTAAC 120  
DB 61 GGGCTGACGAATTCGATCAACGCTTATGATACCGTGCACCTCGAGGGGGGCTAAC 120  
QY 121 TAACTAATTTGTTTGTGGCGCGCGC 149  
121 TAACTAATTTGTTTGTGGCGCGCGC 149  
DB 121 TAACTAATTTGTTTGTGGCGCGCGC 149

RESULT 3  
US-09-822-250-9  
Sequence 9, Application US/09822250  
Patent No. US20020018785A1  
GENERAL INFORMATION:  
APPLICANT: Zauderer, Maurice  
TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus  
FILE REFERENCE: 1821.0010001  
CURRENT APPLICATION NUMBER: US/09/822,250  
CURRENT FILING DATE: 2001-04-02  
PRIOR APPLICATION NUMBER: US 08/935,377  
PRIOR FILING DATE: 1997-09-22  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 9  
LENGTH: 150  
TYPE: DNA  
ORGANISM: synthetic construct  
US-09-822-250-9

Query Match 92.6%; Score 138; DB 10; Length 150;  
Best Local Similarity 99.3%; Pred. No. 1.6e-42;  
Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGGCAAAATTTGAAAATCTATTTATTTGACGCGCGCCCATGA-GTGGATCCCC 59  
1 GGGCAAAATTTGAAAATCTATTTATTTGACGCGCGCCCATGAGTGCATCCCC 60  
DB 1 GGGCAAAATTTGAAAATCTATTTATTTGACGCGCGCCCATGAGTGCATCCCC 60  
QY 60 GGGCTGACGAATTCGATCAACGCTTATGATACCGTGCACCTCGAGGGGGGCTAAC 119  
119 GGGCTGACGAATTCGATCAACGCTTATGATACCGTGCACCTCGAGGGGGGCTAAC 119

DB 61 GGGCTGACGAATTCGATCAACGCTTATGATACCGTGCACCTCGAGGGGGGCTAAC 120  
QY 120 CTAACATAATTTGTTTGTGGCGCGCGC 149  
120 CTAACATAATTTGTTTGTGGCGCGCGC 149  
DB 121 CTAACATAATTTGTTTGTGGCGCGCGC 150  
121 CTAACATAATTTGTTTGTGGCGCGCGC 150

RESULT 4  
US-09-987-456-5  
Sequence 5, Application US/09987456  
Patent No. US20020123057A1  
GENERAL INFORMATION:  
APPLICANT: University of Rochester  
APPLICANT: Zauderer, Maurice  
APPLICANT: Ernest S. Smith  
TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting  
TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells  
FILE REFERENCE: 1821.0070004  
CURRENT APPLICATION NUMBER: US/09/987,456  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/271,424  
PRIOR FILING DATE: 2001-02-27  
PRIOR APPLICATION NUMBER: 60/262,067  
PRIOR FILING DATE: 2001-01-18  
PRIOR APPLICATION NUMBER: 60/298,087  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/249,268  
PRIOR FILING DATE: 2000-11-17  
NUMBER OF SEQ ID NOS: 147  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 150  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: p7.5/ATG3/lk vector  
US-09-987-456-5

Query Match 92.6%; Score 138; DB 10; Length 150;  
Best Local Similarity 99.3%; Pred. No. 1.6e-42;  
Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGGCAAAATTTGAAAATCTAGATCTATTTATTTGACGCGCGCCCATGA-GTGGATCCCC 59  
1 GGGCAAAATTTGAAAATCTAGATCTATTTATTTGACGCGCGCCCATGAGTGCATCCCC 60  
DB 1 GGGCAAAATTTGAAAATCTAGATCTATTTATTTGACGCGCGCCCATGAGTGCATCCCC 60  
QY 60 GGGCTGACGAATTCGATCAACGCTTATGATACCGTGCACCTCGAGGGGGGCTAAC 119  
61 GGGCTGACGAATTCGATCAACGCTTATGATACCGTGCACCTCGAGGGGGGCTAAC 120  
DB 61 GGGCTGACGAATTCGATCAACGCTTATGATACCGTGCACCTCGAGGGGGGCTAAC 120  
QY 120 CTAACATAATTTGTTTGTGGCGCGCGC 149  
120 CTAACATAATTTGTTTGTGGCGCGCGC 149  
DB 121 CTAACATAATTTGTTTGTGGCGCGCGC 150  
121 CTAACATAATTTGTTTGTGGCGCGCGC 150

RESULT 5  
US-09-822-250-7  
Sequence 7, Application US/09822250  
Patent No. US20020018785A1  
GENERAL INFORMATION:  
APPLICANT: Zauderer, Maurice  
TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus  
FILE REFERENCE: 1821.0010001  
CURRENT APPLICATION NUMBER: US/09/822,250  
CURRENT FILING DATE: 2001-04-02  
PRIOR APPLICATION NUMBER: US 08/935,377  
PRIOR FILING DATE: 1997-09-22  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 7  
LENGTH: 148  
TYPE: DNA  
ORGANISM: synthetic construct



US-09-822-250-7

Query Match	91.9%;	Score 137;	DB 10;	Length 148;
Best Local Similarity	99.3%;	Pred. No. 3.7e-42;		
Matches 148;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1;

**OY**    1 GGGCAAAATTTGAAAACCTAGACTTATTATTTGCAGCGGGCCGCCAAGTGATCCCCC 60  
**Dd**    1 GGCCAAAAATTGAAAACCTAGACTTATTATTTGCAGCGGGCCGCCAAG-TGTGATCCCCC 59

9y 61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAAC 120  
 |||||  
 60 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCGCTAAC 119  
 Db

QY	121 TAACTAATTTGTTTGTGGGCCCGCC	149
Db	120 TAACTAATTTGTTTGTGGGCCCGCC	148

## RESULT 6

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? Sequence 3, Application US/09987456
? Patent No. US20020123057A1
? GENERAL INFORMATION:
? APPLICANT: University of Rochester
? APPLICANT: Zauderer, Maurice
? APPLICANT: Ernest S. Smith
? TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
? TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
? FILE REFERENCE: 1821.0070004
? CURRENT APPLICATION NUMBER: US/09/987,456
? PRIOR FILING DATE: 2001-11-14
? PRIOR APPLICATION NUMBER: 60/271,424
? PRIOR FILING DATE: 2001-02-27
? PRIOR APPLICATION NUMBER: 60/262,067
? PRIOR FILING DATE: 2001-01-18
? PRIOR APPLICATION NUMBER: 60/288,087
? PRIOR FILING DATE: 2001-06-15
? PRIOR APPLICATION NUMBER: 60/249,268
? PRIOR FILING DATE: 2000-11-17
? NUMBER OF SEQ ID NOS: 147
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 3
? LENGTH: 148
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: p 7.5/ATGI/tk promoter
?-S-09-987-456-3

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Query Match	91.98;	Score 137;	DB 10;	Length 148;
Best Local Similarity	99.38;	Pred. No. 3.7e-42;		
Matches 148; Conservative	0;	Mismatches 0;	Indels 1;	Gaps 1;

[illegible]

QY	121	TAAC	TA	TT	GT	TT	GT	GG	CC	GG	CC	149
Db	120	TAAC	TA	TT <td>GT <td>TT <td>GT <td>GG</td> <td>CC</td> <td>GG</td> <td>CC</td> <td>148</td> </td></td></td>	GT <td>TT <td>GT <td>GG</td> <td>CC</td> <td>GG</td> <td>CC</td> <td>148</td> </td></td>	TT <td>GT <td>GG</td> <td>CC</td> <td>GG</td> <td>CC</td> <td>148</td> </td>	GT <td>GG</td> <td>CC</td> <td>GG</td> <td>CC</td> <td>148</td>	GG	CC	GG	CC	148

RESULT 7  
US-09-822-250-6

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RESULT 7
US-09-822-250-6
; Sequence 6, Application US/09822250
; Patent No. US20020018785a1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice

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; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1831 0010001

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FILE REFERENCE: 1821.0010001

; CURRENT APPLICATION NUMBER: US/09/822,250

CURRENT FILING DATE: 2001-04-02

PRIOR APPLICATION NUMBER: US 08/935,377

PRIOR FILING DATE: 1997-09-22

NUMBER OF SEQ ID NOS: 37

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; SOFTWARE: Patentlin version 3.0
; CEO ID NO 6

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; SEQ ID NO 6  
: LENGTH: 145

TYPE: DNA  
LENGTH: 143

TYPE: DNA  
ORGANISM: *S. aureus*

US-09-822-250-6

007060

Query Match	87.9%;	Score 131;	DB 10;	Length 145;
Best Local Similarity	97.3%;	Pred. No. 6.6e-40;		
Matches 145;	Conservative	0;	Mismatches	0; Indels 4; Gaps 1

Dy 1 GGCCAAAATTGAAAACTAGATCTATTTATTCACGGCGGCCCATGTGGATCCCC 60  
|||||  
|||  
Dp 1 GGCCAAAATTGAAAACTAGATCTATTTATTCACGGCGGCC---GTGGATCCCC 56

QY 61 GGGCTGCAGGAATTGCATATCAAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAAC 120  
|||||  
Dp 57 GGGCTGCAGGAATTGCATATCAAGCTTATCGATACCGTGCACCTCGAGGGGGGCGCTAAC 116  
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QY	121	TAACTAATTTGTTTTGTGGCCCGGCC	149
Db	117	TAACTAATTTGTTTTGTGGCCCGGCC	145

RESULT 8  
US-09-987-456-2

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? Sequence 2, Application US/09987456
? Patent No. US20020123057A1
?
? GENERAL INFORMATION:
?
? APPLICANT: University of Rochester
?
? APPLICANT: Zanderer, Maurice
?
? APPLICANT: Ernest S. Smith
?
? TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
?
? TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
?
? FILE REFERENCE: 1821.0070004
?
? CURRENT APPLICATION NUMBER: US/09/987,456
?
? PRIOR FILING DATE: 2001-11-14
?
? PRIOR APPLICATION NUMBER: 60/271,424
?
? PRIOR FILING DATE: 2001-02-27
?
? PRIOR APPLICATION NUMBER: 60/262,067
?
? PRIOR FILING DATE: 2001-01-18
?
? PRIOR APPLICATION NUMBER: 60/298,087
?
? PRIOR FILING DATE: 2001-06-15
?
? PRIOR APPLICATION NUMBER: 60/249,268
?
? PRIOR FILING DATE: 2000-11-17
?
? NUMBER OF SEQ ID NOS: 147
?
? SOFTWARE: Patentin version 3.1
?
? SEQ ID NO 2
?
? LENGTH: 145
?
? TYPE: DNA
?
? ORGANISM: Artificial Sequence
?
? FEATURE:
?
? OTHER INFORMATION: p 7.5/ATGCo/tk promoter
?
?-S-09-987-456-2

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Query Match	87.9%	Score 131;	DB 10;	Length 145;
Best Local Similarity	97.3%;	Pred. No. 6.6e-40;		
Matches 145; Conservative	0;	Mismatches 0;	Indels 4;	Gaps 1;

QY 1 GGCCAAAATTGAAAACCTAGATCTATTATTATTCACGCGGCCCATGAGTGGATCCCC 60  
|||||  
Db 1 GGCCAAAATTGAAAACCTAGATCTATTATTATTCACGCGGCCCGCC---GTGGATCCCC 56

QY 61 GGGCTGCAGGAATTGCATATCAAGCTTATCGATTACCGTCGACCTCGAGGGGGGGCCTAAC 120  
|||||  
Db 57 GGGCTGCAGGAATTGCATATCAAGCTTATCGATTACCGTCGACCTCGAGGGGGGGCCTAAC 116

Oy	121 TAACATAATTTGTTTTGTGGCCCGGCC	149
Db	117 TAACATAATTTGTTTTGTGGCCCGGCC	145

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RESULT 9
US-09-834-975-601/c
Sequence 601, Application US/09834975
Patent No. US20020110815A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
APPLICANT: Bolt, Andrew
APPLICANT: Van Huuffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
OF HUMAN CANCERS
FILE REFERENCE: MRI-016B
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
PRIORITY FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 601
LENGTH: 424
TYPE: DNA
ORGANISM: Homo sapiens
US-09-834-975-601

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	Query Match	Similarity	88.4%	Score 70:	DB 10:	Length 424:
	Best Local	Similarity	88.4%	Pred. No. 8:	8e-17:	
	Matches	76:	Conservative	0:	Mismatches 10:	Indels 0:
						Gaps 0:
QY	49	ATGTGATCCCCCGGGCTGAGAGATTCGATATCAACGTTATGATACCTCGACCTCGAG	108			
DB	105	ATGTGATCCCCCGGGCTGAGAGATTCGATATCAACGTTATGATACCTCGACCTCGAG	46			
QY	109	GGGGGGCCTAACTAATATTTTGT	134			
DB	45	GGGGGGCCCGGTACCAACGCTTTTGT	20			

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/ RESULT 10
/ US-09-735-705-91
/ Sequence 91, Application US/09735705
/ Patent No. US20020052329A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tonglong
/ APPLICANT: Fan, Liqun
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Hosken, Nancy
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Li, Samuel X.
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skelky, Yasir A.W.
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: McNeill, Patricia D.
/ APPLICANT: Fanger, Neil
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.455C14
/ CURRENT APPLICATION NUMBER: US/09/735,705
/ CURRENT FILING DATE: 2000-12-12
/ NUMBER OF SEQ ID NOS: 419
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 91
/ LENGTH: 858
/ TYPE: DNA
/ ORGANISM: Homo sapien
/ FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: (1)..(858)
; OTHER INFORMATION: n = A,T,C or G
US-09-735-705-91
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[illegible]

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US-09-850-716A-91
; RESULT 11
; Sequence 91 Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Relfer, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 91
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(858)
; OTHER INFORMATION: n = A,T,C or G
US-09-850-716A-91

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Query Match	46.6%;	Score 69.4;	DB 10;	Length 858;
Best Local Similarity	76.6%;	Pred. No. 2e-16;		
Matches	85;	Conservative	0;	Mismatches 26;
			Indels	0;
			Gaps	0;

QY 6 AAATTTGAAAACTGACATCTATTATTCAGCGGGCCGCATGTGATGCCCGGGCT 65  
| | | | |  
Db 313 AATAATCTCACCGGAGATTCAACGANATTCACACCATCTGGACTGTGATGCCCGGGCT 373 Z  
| | | | |  
QY 66 GCAGGAATTCGATCAAGCTTATTCGATACCGTCGACCTCGAGGGGGGGCCC 116  
| | | | |  
Db 373 GCAGGAATTCGATCAAGCTTATTCGATACCGTCGACCTCGAGGGGGGGGGC 423

RESULT 12 778-91  
 ; Sequence 91, Application US/09897778  
 ; Patent No. US20020147143A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Tongtong  
 ; APPLICANT: Marnerakis, Margarita  
 ; APPLICANT: Fanger, Gary R.  
 ; APPLICANT: Vedovick, Thomas S.  
 ; APPLICANT: Carter, Darrick  
 ; APPLICANT: Watanabe, Yoshihiro  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: Peckham, David W.  
 ; APPLICANT: Fanger, Neil  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.455C16

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; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 570, 591, 655, 664, 667, 683, 711, 759, 760, 765, 777, 787,
; LOCATION: 792, 794, 801, 804, 809, 817, 820
; OTHER INFORMATION: n - A,T,C or G
US-09-897-778-91
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Query Match
Best Local Similarity 46.6%; Score 69.4; DB 10; Length 858;
Matches 85; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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QY 6 AAAATTGAAACTAGATCTATTATTGACGGCGCCGCAATGATGATCCCGGGCT 65
Db 313 ATATATCTCACGAGGATTCACAGATTCACACACTGACTAGTGGATCCCGGGCT 372
QY 66 GCAGGATTCGATATCAAGCTTATCGATACCGTCACTCGAGGGGGGCC 116
Db 373 GCAGGATTCGATATCAAGCTTATCGATACCGTCACTCGAGGGGGGCC 423
```

## RESULT 13

```

; Sequence 306, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 306
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-735-705-306
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```

Query Match
Best Local Similarity 46.0%; Score 68.6; DB 10; Length 457;
Matches 71; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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```

QY 42 CGCCATGATGATCCCGGGCTGCAGAAATTCATATCAAGCTTATCGATACCGTCA 101
Db 352 CACAACTAGTGGATCCCGGGCTGCAGAAATTCATATCAAGCTTATCGATACCGTCA 411
QY 102 CCTCGAGGGGGGCC 116
Db 412 CCTCGAGGGGGGCC 426
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## RESULT 14

US-09-850-716A-306

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; Sequence 306, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 306
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-850-716A-306
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```

Query Match
Best Local Similarity 46.0%; Score 68.6; DB 10; Length 457;
Matches 71; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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```

QY 42 CGCCATGATGATCCCGGGCTGCAGAAATTCATATCAAGCTTATCGATACCGTCA 101
Db 352 CACAACTAGTGGATCCCGGGCTGCAGAAATTCATATCAAGCTTATCGATACCGTCA 411
QY 102 CCTCGAGGGGGGCC 116
Db 412 CCTCGAGGGGGGCC 426
```

## RESULT 15

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; Sequence 306, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Marnetakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 306
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-897-778-306
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```

Query Match
Best Local Similarity 46.0%; Score 68.6; DB 10; Length 457;
Matches 71; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```

QY 42 CGCCATGATGATCCCGGGCTGCAGAAATTCATATCAAGCTTATCGATACCGTCA 101
Db 352 CACAACTAGTGGATCCCGGGCTGCAGAAATTCATATCAAGCTTATCGATACCGTCA 411
QY 102 CCTCGAGGGGGGCC 116
Db 412 CCTCGAGGGGGGCC 426
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Search completed: November 10, 2002, 11:33:46

Tue Nov 12 06:25:43 2002

us-08-935-377-8.rnpb

Page 6

Job time : 37.0825 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:43:30 ; Search time 38.1994 Seconds

(Without alignments)  
1196.219 Million cell updates/sec

Title: US-08-935-377-8

Sequence: 1 GGGCAAAATTTGAAAACTA.....TTGTTTGTGGCCCGGCC 149

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PTCUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfillseq1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	47.0	229	US-08-116-492A-39	Sequence 39, App1
2	69.4	46.6	858	US-09-123-912-91	Sequence 91, App1
3	69.4	46.6	858	US-09-643-597-91	Sequence 91, App1
4	68.6	46.0	457	US-09-643-597-306	Sequence 306, App1
5	68	45.6	147	US-09-323-872A-26	Sequence 26, App1
6	68	45.6	752	US-08-976-359-108	Sequence 108, App1
7	68	45.6	2961	US-08-446-935-6	Sequence 6, App1
8	68	45.6	3792	US-08-992-334-1	Sequence 1, App1
9	68	45.6	3792	US-08-302-752-1	Sequence 1, App1
10	68	45.6	4016	US-08-410-540-3	Sequence 3, App1
11	68	45.6	5234	US-08-992-334-2	Sequence 2, App1
12	68	45.6	5592	US-08-302-752-2	Sequence 2, App1
13	68	45.6	6722	US-08-982-334-3	Sequence 3, App1
14	68	45.6	6722	US-08-982-334-3	Sequence 3, App1
15	68	45.6	6722	US-08-982-334-3	Sequence 3, App1
16	67.8	45.5	545	US-08-991-789A-10	Sequence 10, App1
17	67.8	45.5	545	US-09-062-451-10	Sequence 10, App1
18	67.8	45.5	545	US-09-598-326-10	Sequence 10, App1
19	67.8	45.5	793	US-08-967-101-121	Sequence 121, App1
20	67.8	45.5	793	US-08-582-541-121	Sequence 121, App1
21	67.8	45.5	793	US-09-124-698-121	Sequence 121, App1
22	67.8	45.5	793	US-09-127-480-121	Sequence 121, App1
23	67.8	45.5	793	US-08-496-841C-121	Sequence 121, App1
24	67.8	45.5	793	US-09-124-523-121	Sequence 121, App1
25	66.2	44.4	3481	US-09-462-645C-11	Sequence 11, App1
26	66.2	44.4	3810	US-09-462-645C-7	Sequence 7, App1
27	66	44.3	11233	US-08-980-832-27	Sequence 27, App1

C	28	65.4	43.9	5356	4	US-08-446-935-1	Sequence 1, App1
C	29	65.4	43.9	718	2	US-08-793-610-6	Sequence 6, App1
C	30	65	43.6	938	4	US-09-462-645C-25	Sequence 25, App1
C	31	65	43.6	84	4	US-09-462-645C-26	Sequence 26, App1
C	32	65	43.6	698	4	US-08-998-416-54	Sequence 54, App1
C	33	65	43.6	3465	4	US-08-462-645C-9	Sequence 9, App1
C	34	65	43.6	3794	4	US-09-462-645C-5	Sequence 5, App1
C	35	65	43.6	6596	4	US-09-575-602-11	Sequence 11, App1
C	36	64.4	43.2	713	4	US-08-998-416-135	Sequence 135, App1
C	37	63.4	42.6	685	1	US-08-463-115-56	Sequence 56, App1
C	38	63.4	42.6	685	1	US-08-465-388-56	Sequence 56, App1
C	39	60	40.3	4164	1	US-08-204-675-1	Sequence 1, App1
C	40	60	40.3	4164	2	US-08-660-754-1	Sequence 1, App1
C	41	60	40.3	4164	2	US-08-796-364-1	Sequence 1, App1
C	42	60	40.3	4164	5	PCT-US95-02520-1	Sequence 1, App1
C	43	60	40.3	5178	2	US-08-474-169-2	Sequence 2, App1
C	44	58.8	39.5	3198	4	US-08-842-306B-48	Sequence 48, App1
C	45	58.8	39.5	3198	4	US-08-838-973B-48	Sequence 48, App1

#### ALIGNMENTS

```
RESULT 1
US-09-116-492A-39/c
; Sequence 39, Application US/09116492A
; Patent No. 6436409
; GENERAL INFORMATION:
; APPLICANT: GICOUEL, BRIGITTE
; APPLICANT: BERTHET, FRANCOIS-XAVIER
; APPLICANT: ANDERSEN, PETER
; APPLICANT: RASMUSSEN, PETER B
; TITLE OF INVENTION: POLYNUCLEOTIDE FUNCTIONALLY CODING FOR THE LHP PROTEIN FROM MY
; TITLE OF INVENTION: TUBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGMENTS, A
; FILE REFERENCE: 0660-0137-27X
; CURRENT APPLICATION NUMBER: US/09/116,492A
; CURRENT FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 60/252,631
; PRIOR FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: multiple cloning site-artificial DNA
US-09-116-492A-39

Query Match      47.0%; Score 70; DB 4; Length 229;
Best Local Similarity 88.4%; Pred. No. 1.3e-15;
Matches 76; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 49 AGGAGATCCCGGGCGTGCAGATTCGATACGATACCTGACCTGCAGC 108
    |||||||
DB 141 AGGAGATCCCGGGCGTGCAGATTCGATACGATACCTGACCTGCAGC 82
    |||||||
OY 109 GGGGGGCTACTACTACTATTTGTT 134
    |||||||
DB 81 GGGGGGCGCGGTACCCAGCTTTGTT 56

RESULT 2
US-09-123-912-91
; Sequence 91, Application US/09123912A
; Patent No. 6312695
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongcong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
; FILE REFERENCE: 210121.455C1
; CURRENT APPLICATION NUMBER: US/09/123,912A
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CURRENT FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: 09/040,802
PRIOR FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 91
LENGTH: 858
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (570)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (591)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (655)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (664)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (667)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (683)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (711)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (759)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (760)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (765)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (777)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (787)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (792)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (794)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (801)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (804)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (809)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (817)
OTHER INFORMATION: where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (820)
OTHER INFORMATION: where n is a, c, g or t
US-09-123-912-91
Query Match      46.6%; Score 69.4; DB 4; Length 858;
Best Local Similarity 76.6%; Pred. No. 3.3e-15;
Matches 85; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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OY      6 AAAATTGAAAACACTAGATCTTATTATGGACAGCGGCCGCATGATGTCATCCCGGGGCT 65
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      313 ATATCTCACCAGAGATCAACGAATTCACCACTGCACTGATGTGATGCCCGGGCT 372
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      66 GCAGAGAATTCGATCAACGCTTATCGATTACCGTCGACCTCGAGGGGGGGCC 116
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      373 GCAGAGAATTCGATCAACGCTTATCGATTACCGTCGACCTCGAGGGGGGGCC 423
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
US-09-643-597-91
; Sequence 91, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643.597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 91
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(858)
; OTHER INFORMATION: n = A,T,C or G
US-09-643-597-91

Query Match          46.6%; Score 69.4; DB 4; Length 858;
Best Local Similarity 76.6%; Pred.No.3.e-15;
Matches    85; Conservative   0; Mismatches 26; Indels   0; Gaps   0;

OY      6 AAAATTGAAAACTAGATCTATTATTGTCACGCGGCCGCCCATGATGATCCCCGGGCT 65
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      313 ATATCTCACCGAGATCAACGAATTCACCACTGCACTGATGTGATGCCCGGGCT 372
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      66 GCAGAGAATTCGATCAACGCTTATCGATTACCGTCGACCTCGAGGGGGGGCC 116
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      373 GCAGAGAATTCGATCAACGCTTATCGATTACCGTCGACCTCGAGGGGGGGCC 423
        ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
US-09-643-597-306
; Sequence 306, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; AND DIAGNOSIS OF LUNG CANCER
```

FILE REFERENCE: 210121.455C11  
CURRENT APPLICATION NUMBER: US/09/643,597  
CURRENT FILING DATE: 2000-08-21  
NUMBER OF SEQ ID NOS: 369  
SOFTWARE: FASTSEQ for Windows Version 3.0  
SEQ ID NO 306  
LENGTH: 457  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-643-597-306

Query Match 46.0%; Score 68.6; DB 4; Length 457;  
Best Local Similarity 94.7%; Pred. No. 5.1e-15;  
Matches 71; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 42 CGCGATGATGATCCCGGCGCTGCAGGAAATTCATATCAAGCTTATGATACCGTCGA 101  
DB 352 CACACTAGTGCATCCCGGCGCTGCAGGAAATTCATATCAAGCTTATGATACCGTCGA 411  
QY 102 CCTCGAGGGGGGCC 116  
DB 412 CCTCGAGGGGGGCC 426

RESULT 5  
US-09-323-872A-26/c  
Sequence 26, Application US/09323872A  
Patent No. 6395539  
GENERAL INFORMATION:  
APPLICANT: Coschigano, Peter  
TITLE OF INVENTION: Compositions and Methods for Bioremediation  
FILE REFERENCE: OHU-03640  
CURRENT APPLICATION NUMBER: US/09/323,872A  
CURRENT FILING DATE: 2001-06-15  
PRIOR FILING DATE: 1998-05-04  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 26  
LENGTH: 147  
TYPE: DNA  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(147)  
US-09-323-872A-26

Query Match 45.6%; Score 68; DB 4; Length 147;  
Best Local Similarity 100.0%; Pred. No. 5.6e-15;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AGTGCATCCCGGCGCTGCAGGAAATTCATATCAAGCTTATGATACCGTCGAG 108  
DB 107 AGTGCATCCCGGCGCTGCAGGAAATTCATATCAAGCTTATGATACCGTCGAG 48

QY 109 GGGGGGCC 116  
DB 47 GGGGGGCC 40

RESULT 6  
US-08-976-259-108/c  
Sequence 108, Application US/08976259  
Patent No. 6316609  
GENERAL INFORMATION:  
APPLICANT: Dillon, Patrick J.  
APPLICANT: Choi, Gil H.  
APPLICANT: Welch, Rodney A.  
TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli  
Patent No. 6316609  
NUMBER OF SEQUENCES: 142  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Ave, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/976,259  
FILING DATE: Herewith  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/031,626 AND US 60/061,953  
ATTORNEY/AGENT INFORMATION:  
NAME: Steffe, Eric K. 36,688  
REGISTRATION NUMBER: 1488.0740002/EKS/CBM  
REFERENCE/DOCKET NUMBER: 1488.0740002/EKS/CBM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 752 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-976-259-108

Query Match 45.6%; Score 68; DB 4; Length 752;  
Best Local Similarity 100.0%; Pred. No. 1e-14;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AGTGCATCCCGGCGCTGCAGGAAATTCATATCAAGCTTATGATACCGTCGAG 108  
DB 73 AGTGCATCCCGGCGCTGCAGGAAATTCATATCAAGCTTATGATACCGTCGAG 14  
QY 109 GGGGGGCC 116  
DB 13 GGGGGGCC 6

RESULT 7  
US-08-446-935-6/c  
Sequence 6, Application US/08446935  
Patent No. 6187991  
GENERAL INFORMATION:  
APPLICANT: Soeller, Walter C.  
APPLICANT: Carly, Maynard D.  
APPLICANT: Kreutler, David K.  
TITLE OF INVENTION: TRANSGENIC ANIMAL MODELS FOR TYPE II  
TITLE OF INVENTION: DIABETES MELLITUS  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pfizer Inc.  
STREET: 235 East 42nd Street, 20th Floor  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10017-5755  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,935  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Sheyka, Robert F.

```

;
;   REGISTRATION NUMBER: 31,304
;   REFERENCE/DOCKET NUMBER: PC8153
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212)573-1189
;   TELEFAX: (212)573-1939
;   TELEX: N/A
;   INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 2961 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: circular
;   MOLECULE TYPE: DNA (genomic)
;
US-08-446-935-6

Query Match
Best Local Similarity 45.6%; Score 68; DB 4; Length 2961;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AGTGATCCCCCGGCTGCAGATTCGATTCAGCTTATCGATACCGTCGACCTCGAG 108
Db 727 AGTGATCCCCCGGCTGCAGATTCGATTCAGCTTATCGATACCGTCGACCTCGAG 668
QY 109 GGGGGGCC 116
Db 667 GGGGGGCC 660

RESULT 8
US-08-992-334-1/c
; Sequence 1, Application US/0892334
; Patent No. 5919678
;
GENERAL INFORMATION:
; APPLICANT: Gruss, Alexandra
; APPLICANT: Maguin, Emmanuelle
; TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE
;   NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: Christie Parker & Hale, LLP
; STREET: 350 West Colorado Boulevard, Suite 500
; CITY: Pasadena
; STATE: California
; COUNTRY: United States
; ZIP: 91105
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/992,334
; FILING DATE: 17-DEC-1997
; CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/302,752
; FILING DATE: 24-DEC-1994
;
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00248
; FILING DATE: 12-MAR-1993
; APPLICATION NUMBER: FR 92/03034
; FILING DATE: 13-MAR-1992
;
ATTORNEY/AGENT INFORMATION:
; NAME: Prout, D. Bruce
; REGISTRATION NUMBER: 20958
; REFERENCE/DOCKET NUMBER: C93:31779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 795-9900
; TELEFAX: (626) 577-8800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3792 base pairs
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;
;   TYPE: nucleic acid
;   STRANDEDNESS: both
;   TOPOLOGY: circular
;   MOLECULE TYPE: DNA (genomic)
;   HYPOTHETICAL: NO
;   ANTI-SENSE: YES
;   IMMEDIATE SOURCE:
;   CLONE: pg+host4
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US-08-992-334-1

Query Match
Best Local Similarity 45.6%; Score 68; DB 2; Length 3792;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AGTGATCCCCCGGCTGCAGATTCGATTCAGCTTATCGATACCGTCGACCTCGAG 108
Db 3542 AGTGATCCCCCGGCTGCAGATTCGATTCAGCTTATCGATACCGTCGACCTCGAG 3483
QY 109 GGGGGGCC 116
Db 3482 GGGGGGCC 3475

RESULT 9
US-08-302-752-1/c
; Sequence 1, Application US/08302752
; Patent No. 6025190
;
GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THERMOSENSIBLE PLASMID
; NUMBER OF SEQUENCES: 3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
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CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,752
; FILING DATE:
; CLASSIFICATION: 435
;
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9203034
; FILING DATE: 13-MAR-1992
;
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR/93/00248
; FILING DATE: 12-MAR-1993
;
INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3792 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-302-752-1

Query Match
Best Local Similarity 45.6%; Score 68; DB 3; Length 3792;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AGTGATCCCCCGGCTGCAGATTCGATTCAGCTTATCGATACCGTCGACCTCGAG 108
Db 3542 AGTGATCCCCCGGCTGCAGATTCGATTCAGCTTATCGATACCGTCGACCTCGAG 3483
QY 109 GGGGGGCC 116
Db 3482 GGGGGGCC 3475

RESULT 10
US-08-410-540-3
; Sequence 3, Application US/08410540
; Patent No. 5807678
;
GENERAL INFORMATION:
```



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APPLICANT: Miller, Walter L.
APPLICANT: Lin, Dong
TITLE OF INVENTION: STRAUS III, Jerome F.
TITLE OF INVENTION: IDENTIFICATION OF GENE MUTATIONS
TITLE OF INVENTION: ASSOCIATED WITH CONGENITAL LIPOID ADRENAL HYPERPLASIA
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,540
FILING DATE: 23-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard L.
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: UCAL-238/00US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 853 5070
TELEFAX: 415 857 0663
TELEX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4016 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: exon
LOCATION: 1098..1283
FEATURE:
NAME/KEY: exon
LOCATION: 1620..1733
FEATURE:
NAME/KEY: exon
LOCATION: 2047..2174
FEATURE:
NAME/KEY: exon
LOCATION: 2267..2425
FEATURE:
NAME/KEY: exon
LOCATION: 2567..2751
FEATURE:
NAME/KEY: exon
LOCATION: 2828..2921
FEATURE:
NAME/KEY: exon
LOCATION: 3031..3765
FEATURE:
NAME/KEY: 1433..1434
OTHER INFORMATION: /note= "interruption of sequence data"
FEATURE:
NAME/KEY: 2208..2209
OTHER INFORMATION: /note= "interruption of sequence data"
FEATURE:
NAME/KEY: 2781..2782
OTHER INFORMATION: /note= "interruption of sequence data"
FEATURE:

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NAME/KEY: -
LOCATION: 2956..2957
OTHER INFORMATION: /note= "interruption of sequence data"
US-08-410-540-3
Query Match
Best Local Similarity 45.6%; Score 68; DB 1; Length 4016;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 49 AGTGATCCCCGGGCTGCAGATTCGATCAAGCTTATCGATACCTGACCTGAG 108
DB 3938 AGTGATCCCCGGGCTGCAGATTCGATTCAGCTTATCGATACCTGACCTGAG 3997
QY 109 GGGGGGCC 116
DB 3998 GGGGGGCC 4005

```

```

RESULT 11
US-08-992-334-2/C
Sequence 2, Application US/08992334
Patent No. 5919678
GENERAL INFORMATION:
APPLICANT: Gruss, Alexandra
TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE
TITLE OF INVENTION: PLASMID
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christie Parker & Hale, LLP
STREET: 350 West Colorado Boulevard, Suite 500
CITY: Pasadena
STATE: California
COUNTRY: United States
ZIP: 91105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/992,334
FILING DATE: 17-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,752
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00248
FILING DATE: 12-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 992/03034
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Proulx, D. Bruce
REGISTRATION NUMBER: 20958
REFERENCE/DOCKET NUMBER: C93:31779
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 795-9900
TELEFAX: (626) 577-8800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5234 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
US-08-992-334-2

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Query Match 45.6%; Score 68; DB 2; Length 5234;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	49	AGTGGATATCCCCGGGGCTGCAGAAATTCGATATCAAGCTTATGATACCGTGTACCTCGAG	108
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QY	109	GGGGGGGCC	116
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US-08-302-752-2          RESULT 12
; Sequence 2, Application US/08302752
; Patent No. 6025190
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THERMOSENSIBLE PLASMID
; NUMBER OF SEQUENCES: 3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,752
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9203034
; FILING DATE: 13-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR/93/00248
; FILING DATE: 12-MAR-1993
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5234 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-302-752-2

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: RESULT 13
: US-09-495,797-37
: Sequence 37, Application US/09495797
: Patent No. 6369296
: GENERAL INFORMATION:
: APPLICANT: Ratcliff, Frank G
: APPLICANT: Martin-Hernandez, Ana M
: APPLICANT: Baulcombe, David C
: TITLE OF INVENTION: Viral Vectors
: FILE REFERENCE: Newburn 43,047
: CURRENT APPLICATION NUMBER: US/09/495,797
: CURRENT FILING DATE: 2000-02-01
: NUMBER OF SEQ ID NOS: 46
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 37
: LENGTH: 5592
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
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: OTHER INFORMATION: ptv00
US-09-495-797-37

Query Match          45.6%; Score 68; DB 4; Length 5592;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AGTGAATCCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
      |||||||
DB 2550 AGTGAATCCCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 2609

QY 109 GGGGGGCC 116
      |||||||
DB 2610 GGGGGGCC 2617

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US-08-992-334-3/c
; Sequence 3, Application US/08992334
; Patent No. 5919678
; GENERAL INFORMATION:
; APPLICANT: Gruss, Alexandra
; APPLICANT: Maguin, Emmanuelle
; TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE
; TITLE OF INVENTION: PLASMID
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christie Parker & Hale, LLP
; STREET: 350 West Colorado Boulevard, Suite 500
; CITY: Pasadena
; STATE: California
; COUNTRY: United States
; ZIP: 91105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/992,334
; FILING DATE: 17-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/302,752
; FILING DATE: 24-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00248
; FILING DATE: 12-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 892/03034
; FILING DATE: 13-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Prout, D. Bruce
; REGISTRATION NUMBER: 20958
; REFERENCE/DOCKET NUMBER: C93:31779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 795-9900
; TELEFAX: (626) 577-8800
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6722 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
;
US-08-992-334-3
;
Query Match 45.6%; Score 68; DB 2; Length 6722;
Best Local Similarity 100.0%; Pred.No. 2.1e-14;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0
49 AAGGATGCCCGGGCTGACGAAATTCGATTCACCTTATGATGATCGGACGACGAG 108
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Db 6472 AGTGGATCCCGGGGCTGAGGATTGCATATCAAGCTTATCGATACCGTCGACCTCGAG 6413  
QY 109 GGGGGGCC 116  
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Db 6412 GGGGGGCC 6405

## RESULT 15

US-08-302-752-3/c  
; Sequence 3, Application US/08302752  
; Patent No. 6025190  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: THERMOSENSIBLE PLASMID  
; NUMBER OF SEQUENCES: 3  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA: US/08/302.752  
; APPLICATION NUMBER: US/08/302.752  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 9203034  
; FILING DATE: 13-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO FR/93/00248  
; FILING DATE: 12-MAR-1993  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6722 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-302-752-3

Query Match 45.6%; Score 68; DB 3; Length 6722;  
Best Local Similarity 100.0%; Pred. No. 2.1e-14;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 6472 AGTGGATCCCGGGGCTGAGGATTGCATATCAAGCTTATCGATACCGTCGACCTCGAG 6413  
QY 109 GGGGGGCC 116  
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Db 6412 GGGGGGCC 6405

Search completed: November 10, 2002, 08:36:20  
Job time : 44.1994 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:05:45 ; Search time 729.31 Seconds

(without alignments)  
5985.683 Million cell updates/sec

Title: US-08-935-377-9

Sequence: 1 GGCAGAAATGAAAACTA.....TTGTTTGTGGGCGCGCC 150

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb\_htg:\*  
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11: gb\_sts:\*  
12: gb\_sy:\*  
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14: gb\_vl:\*  
15: em\_da:\*  
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40: em\_htg\_mus:\*  
41: em\_htg\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	150	100.0	150	6	AX326746
2	138	92.0	149	6	AX326745
3	136	90.7	148	6	AX326744
4	130	86.7	145	6	AX326743
5	72.2	48.1	855	6	AX461060
6	69.8	46.5	793	6	AR060142
7	69.8	46.5	793	6	AR087297
8	69.8	46.5	793	6	AR144844
9	69.8	46.5	793	6	AR144585
10	69.8	46.5	13558	6	AX287041
11	69	46.0	259	6	A44281
12	69	46.0	424	6	AX284796
13	69	46.0	2059	12	AY034154
14	69	46.0	2890	9	AB035274
15	69	46.0	2958	12	AB035274
16	69	46.0	2958	12	AB035274
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ALIGNMENTS

RESULT 1  
LOCUS AX326746 150 bp DNA  
DEFINITION Sequence 7 from Patent WO0172995.  
ACCESSION AX326746  
VERSION AX326746.1 GI:18097472  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1  
Zauderer, M. and Smith, E.S.  
Methods of producing a library and methods of selecting  
polynucleotides of interest  
Patent: WO 01/72995-A 7 04-OCT-2001;

UNIVERSITY OF ROCHESTER (US)									
FEATURES	Location/Qualifiers								
Source	1..150								
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	/db_xref="taxon:32630"								
	/note="Nucleotide Sequence of p7.5/AmG3/Lk"								
BASE COUNT	36 a 38 c 39 g 37 t								
ORIGIN									
Query Match	100.0%; Score 150; DB 6; Length 150;								
Best Local Similarity	100.0%; Pred. No. 1.6e-38;								
Matches 150; Conservative 0;	Mismatches 0; Indels 0; Gaps 0;								
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QY	61 CGGGCTGCAGGAATTCGATATCAACCTTATCGATACCGTCGAGGGGGGCGCTAA 120								
Db	61 CGGGCTGCAGGAATTCGATATCAACCTTATCGATACCGTCGAGGGGGGCGCTAA 120								
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Db	121 CTAACTAATTTGTTTGTGGGGCCGGCC 150								
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LOCUS	AX326745 149 bp								
DEFINITION	Sequence 6 from Patent W00172995.								
ACCESSION	AX326745								
VERSION	AX326745.1 GI:18097471								
KEYWORDS	.								
SOURCE	synthetic construct.								
ORGANISM	synthetic construct								
REFERENCE	artificial sequences.								
AUTHORS	1								
TITLE	Zauderer,M. and Smith,E.S.								
JOURNAL	Methods of producing a library and methods of selecting								
	polynucleotides of interest								
	Patent: WO 0172995-A 6 04-Oct-2001;								
	UNIVERSITY OF ROCHESTER (US)								
FEATURES	Location/Qualifiers								
Source	1..149								
	/organism="synthetic construct"								
	/db_xref="taxon:32630"								
	/note="Nucleotide Sequence of p7.5/AmG2/Lk"								
BASE COUNT	36 a 37 c 39 g 37 t								
ORIGIN									
Query Match	92.0%; Score 138; DB 6; Length 149;								
Best Local Similarity	99.3%; Pred. No. 1.4e-34;								
Matches 149; Conservative 0;	Mismatches 0; Indels 1; Gaps 1;								
QY	1 GGGCAAAATTAAGAACTAGATCTATTATTCAGCGGGCCGCCATGACGTGATCCCC 60								
Db	1 GGGCAAAATTAAGAACTAGATCTATTATTCAGCGGGCCGCCATGACGTGATCCCC 59								
QY	61 CGGGCTGCAGGAATTCGATATCAACCTTATCGATACCGTCGAGGGGGGCGCTAA 120								
Db	60 CGGGCTGCAGGAATTCGATATCAACCTTATCGATACCGTCGAGGGGGGCGCTAA 119								
QY	121 CTAACTAATTTGTTTGTGGGGCCGGCC 150								
Db	120 CTAACTAATTTGTTTGTGGGGCCGGCC 149								
RESULT 3									
AX326744	148 bp DNA linear PAT 07-JAN-2002								
LOCUS	AX326744 148 bp								
DEFINITION	Sequence 5 from Patent W00172995.								
ACCESSION	AX326744								
VERSION	AX326744.1 GI:18097470								

	KEYWORDS	synthetic construct.
	SOURCE	synthetic construct
	ORGANISM	artificial sequences.
	REFERENCE	1
	AUTHORS	Zanderer,M. and Smith,E.S.
	TITLE	Methods of producing a library and methods of selecting polynucleotides of interest
	JOURNAL	Patent: WO 0172995-A 5 04-OCT-2001;
	FEATURES	UNIVERSITY OF ROCHESTER (US)
	source	Location/Qualifiers 1..148
		/organism="synthetic construct"
		/db_xref="taxon:32630"
		/note="Nucleotide sequence of p7.5/Ang10/tk"
	BASE COUNT	35 a 37 c 39 g 37 t
	ORIGIN	
	Query Match	90.7%; Score 136; DB 6; Length 148;
	Best Local Similarity	98.7%; Pred. No. 6e-34;
	Matches 148; Conservative	0; Mismatches 0; Indels 2; Gaps 1;
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Db	1	GCGCAAAAATTTAATAAACAGTACTATTATATTCACGGCGGCCCATG--GTGGATCCCC 58
QY	61	CGGGCTGCAGGAATTCGATATCAACCTTATCAGTACCCTCGACCTCGAGGGGGGCGCTAA 120
Db	59	CGGGCTGCAGGAATTCGATATCAACCTTATCAGTACCCTCGACCTCGAGGGGGGCGCTAA 118
QY	121	CTAACTAATTTTGTTTTGTGGGCGCGCC 150
Db	119	CTAACTAATTTTGTTTTGTGGGCGCGCC 148
	RESULT 4	
	AX326743	145 bp DNA linear PAT 07-JAN-2002
	LOCUS	AX326743
	DEFINITION	Sequence 4 from Patent W00172995.
	ACCESSION	AX326743
	VERSION	AX326743.1 GI:18097469
	KEYWORDS	.
	SOURCE	synthetic construct.
	ORGANISM	artificial sequences.
	REFERENCE	1
	AUTHORS	Zanderer,M. and Smith,E.S.
	TITLE	Methods of producing a library and methods of selecting polynucleotides of interest
	JOURNAL	Patent: WO 0172995-A 4 04-OCT-2001;
	FEATURES	UNIVERSITY OF ROCHESTER (US)
	source	Location/Qualifiers 1..145
		/organism="synthetic construct"
		/db_xref="taxon:32630"
		/note="Nucleotide sequence of p7.5/Ang10/tk"
	BASE COUNT	34 a 37 c 38 g 36 t
	ORIGIN	
	Query Match	86.7%; Score 130; DB 6; Length 145;
	Best Local Similarity	96.7%; Pred. No. 6e-32;
	Matches 145; Conservative	0; Mismatches 0; Indels 5; Gaps 1;
QY	1	GCGCCAAATTTGTAATAACAGTACTATTATATGCACGGCGGCCCATGACGTGATPCCC 60
Db	1	GCGCAAAAATTTAATAAACAGTACTATTATATTCACGGCGGCCCATG-----GTGGATCCCC 55
QY	61	CGGGCTGCAGGAATTCGATATCAACCTTATCAGTACCCTCGACCTCGAGGGGGGCGCTAA 120
Db	56	CGGGCTGCAGGAATTCGATATCAACCTTATCAGTACCCTCGACCTCGAGGGGGGCGCTAA 115
QY	121	CTAACTAATTTTGTTTTGTGGGCGCGCC 150

Db 116 CTAACATAATTTTGTGTCGGCCGCC 145

RESULT 5  
AX461060/c AX461060 855 bp DNA linear PAT 08-JUL-2002  
LOCUS Sequence 50 from Patent WO0222823.  
DEFINITION AX461060  
ACCESSION AX461060  
VERSION AX461060.1 GI:21726271  
KEYWORDS  
SOURCE  
ORGANISM  
Eremothecium gossypii.  
Eremothecium gossypii.  
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; Eremotheciaceae; Eremothecium.

REFERENCE  
1 Althoefer, H., Revuelta Doyal, J.L. and Santos, M.  
AUTHORS Proteins involved in the stress response and genes from Ashbya  
TITLE gossypii coding for the same  
JOURNAL Patent: WO 0222823-A 50 21-MAR-2002;  
BASF AKTIENGESSELLSCHAFT (DE)  
FEATURES  
source  
Location/Qualifiers  
1..855  
/organism="Eremothecium gossypii"  
/db\_xref="taxon:33169"  
misc\_feature /note="AGSKN7"  
307..855  
BASE COUNT 177 a 236 c 210 g 219 t 13 others

Query Match  
Best Local Similarity 48.1%; Score 72.2; DB 6; Length 855;  
Matches 86; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 35 ACCGGCCGCATGACGTGATCCCCGGCTGCGAGAAATTCGATCAAGCTTATCGAT 94  
Db 127 ATGAGGTGCTGACGACCGGATCCCCGGCTGCGAGAAATTCGATCAAGCTTATCGAT 68

QY 95 ACCGTGACCTCGAGGGGGGCTTAACATAATTTTGTGTCGGCCGCC 146  
Db 67 ACCGTGACCTCGAGGGGGGCTTAACATAATTTTGTGTCGGCCGCC 16

RESULT 6  
AR060142/c AR060142 793 bp DNA linear PAT 29-SEP-1999  
LOCUS Sequence 121 from patent US 5840540.  
DEFINITION AR060142  
ACCESSION AR060142  
VERSION AR060142.1 GI:5986592  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 793)  
AUTHORS St. George-Hyslop, P.H., Rommens, J.M. and Fraser, P.E.  
TITLE Nucleic acids encoding presenilin II  
JOURNAL Patent: US 5840540-A 121 24-NOV-1998;  
FEATURES  
source  
Location/Qualifiers  
1..793  
/organism="unknown"  
BASE COUNT 162 a 242 c 146 g 229 t 14 others

Query Match  
Best Local Similarity 46.5%; Score 69.8; DB 6; Length 793;  
Matches 80; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 39 GGCCGCATGACGTGATCCCCGGCTGCGAGAAATTCGATCAAGCTTATCGATCG 98  
Db 130 GGAGCCCGCGGGGGGATCCCCGGCTGCGAGAAATTCGATCAAGCTTATCGATCG 71

QY 99 TCGACCTCGAGGGGGGCTTAACATAATTTTGT 135  
Db 70 TCGACCTCGAGGGGGGCTTAACATAATTTTGT 34

RESULT 7  
AR087297/c AR087297 793 bp DNA linear PAT 07-SEP-2000  
LOCUS Sequence 121 from patent US 5986054.  
DEFINITION AR087297  
ACCESSION AR087297  
VERSION AR087297.1 GI:10014060  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 793)  
AUTHORS St. George-Hyslop, P.H., Rommens, J.M. and Fraser, P.E.  
TITLE Genetic sequences and proteins related to Alzheimer's disease  
JOURNAL Patent: US 5986054-A 121 16-NOV-1999;  
FEATURES  
source  
Location/Qualifiers  
1..793  
/organism="unknown"  
BASE COUNT 162 a 242 c 146 g 229 t 14 others

Query Match  
Best Local Similarity 46.5%; Score 69.8; DB 6; Length 793;  
Matches 80; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 39 GGCCGCATGACGTGATCCCCGGCTGCGAGAAATTCGATCAAGCTTATCGATCG 98  
Db 130 GGAGCCCGCGGGGGGATCCCCGGCTGCGAGAAATTCGATCAAGCTTATCGATCG 71

QY 99 TCGACCTCGAGGGGGGCTTAACATAATTTTGT 135  
Db 70 TCGACCTCGAGGGGGGCTTAACATAATTTTGT 34

RESULT 8  
AR134484/c AR134484 793 bp DNA linear PAT 16-MAY-2001  
LOCUS Sequence 121 from patent US 6194153.  
DEFINITION AR134484  
ACCESSION AR134484  
VERSION AR134484.1 GI:14123389  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 793)  
AUTHORS St. George-Hyslop, P.H., Rommens, J.M. and Fraser, P.E.  
TITLE Methods for determining risk of developing Alzheimer's disease by  
JOURNAL detecting mutations in the presenilin 1 (PS-1) gene  
PATENT: US 6194153-A 121 27-FEB-2001;  
FEATURES  
source  
Location/Qualifiers  
1..793  
/organism="unknown"  
BASE COUNT 162 a 242 c 146 g 229 t 14 others

Query Match  
Best Local Similarity 46.5%; Score 69.8; DB 6; Length 793;  
Matches 80; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 39 GGCCGCATGACGTGATCCCCGGCTGCGAGAAATTCGATCAAGCTTATCGATCG 98  
Db 130 GGAGCCCGCGGGGGGATCCCCGGCTGCGAGAAATTCGATCAAGCTTATCGATCG 71

QY 99 TCGACCTCGAGGGGGGCTTAACATAATTTTGT 135  
Db 70 TCGACCTCGAGGGGGGCTTAACATAATTTTGT 34

RESULT 9  
AR144585/c AR144585 793 bp DNA linear PAT 08-AUG-2001  
LOCUS Sequence 121 from patent US 6210919.  
DEFINITION

ACCESSION ARI44585  
VERSION ARI44585.1 GI:15106452  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
Unidentified.  
REFERENCE 1 (bases 1 to 793)  
AUTHORS St. George-Hyslop, P.H., Remmens, J.M. and Fraser, P.E.  
TITLE Genetic sequences and proteins related to Alzheimer's disease  
JOURNAL Patent: US 6210919-A 121 03-APR-2001;  
FEATURES  
Source 1..793  
Location/Qualifiers  
BASE COUNT 162 a 242 c 146 g 229 t 14 others  
ORIGIN  
Query Match 46.5%; Score 69.8; DB 6; Length 793;  
Best Local Similarity 82.5%; Pred. No. 5e-12;  
Matches 80; Conservative 0; Mismatches 17; Indels 0; Gaps 0;  
OY 39 GGGCGCCATGACGTGATCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACG 98  
DB 130 GGAGGCCCGGGGGCGGATCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACG 71  
OY 99 TCGACCTCGAGGGGGGCGCTTAACCTAATTTTGT 135  
DB 70 TCGACCTCGAGGGGGGCGGCTTAACCTAATTTTGT 34  
RESULT 10  
AX287041 13558 bp DNA linear PAT 21-NOV-2001  
LOCUS AX287041  
DEFINITION Sequence 5 from Patent WO0181623.  
ACCESSION AX287041  
VERSION AX287041.1 GI:17049037  
KEYWORDS  
house mouse.  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1  
AUTHORS Goetz, B., Kammandel, B., Kuner, R., Scheek, S. and Hiemisch, H.  
TITLE Novel neuronally expressed protein and use thereof  
JOURNAL Patent: WO 0181623-A 5 01-NOV-2001;  
FEATURES  
Source 1..13558  
Location/Qualifiers  
BASE COUNT 2936 a 3419 c 3606 g 3544 t 53 others  
ORIGIN  
Query Match 46.5%; Score 69.8; DB 6; Length 13558;  
Best Local Similarity 97.3%; Pred. No. 8.4e-12;  
Matches 71; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
OY 45 CARGAGTGTATCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACGCTGAGC 104  
DB 13481 CAGAGCTGTATCCCGGGCTGCAGAAATTCGATATCAAGCTTATCGATACGCTGAGC 13540  
OY 105 TCGAGGGGGGGCC 117  
DB 13541 TCGAGGGGGGGCC 13553  
RESULT 11  
A44281 259 bp DNA linear PAT 07-MAR-1997  
LOCUS A44281  
DEFINITION Sequence 9 from Patent WO9511300.  
ACCESSION A44281  
VERSION A44281.1 GI:2299115  
KEYWORDS  
SOURCE unidentified.

ORGANISM unidentified  
unclassified.  
REFERENCE 1 (bases 1 to 259)  
AUTHORS Chandley, A.C., Kun, M., Sharkey, A.M., Hargreave, T.B. and Cooke, H.J.  
TITLE AZOOSPERMIA IDENTIFICATION AND TREATMENT  
JOURNAL Patent: WO 9511300-A 9 27-APR-1995;  
COMMENT MEDICAL RES COUNCIL (GB)  
Other publication AU 7947794 950508.  
FEATURES  
Source 1..259  
Location/Qualifiers  
BASE COUNT 67 a 58 c 63 g 69 t 2 others  
ORIGIN  
Query Match 46.0%; Score 69; DB 6; Length 259;  
Best Local Similarity 88.2%; Pred. No. 7.5e-12;  
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
OY 51 GTGATCCCGCGGCTGCAGAAATTCGATATCAAGCTTATCGATACGCTGCAGCTGAGG 110  
DB 112 GTGATCCCGCGGCTGCAGAAATTCGATATCAAGCTTATCGATACGCTGCAGCTGAGG 53  
OY 111 GGGGGCTTAACCTAATTTTGT 135  
DB 52 GGGGGCGCGGTACCCAGCTTTTGT 28  
RESULT 12  
AX284796/c 424 bp DNA linear PAT 20-NOV-2001  
LOCUS AX284796  
DEFINITION Sequence 601 from Patent WO0179556.  
ACCESSION AX284796  
VERSION AX284796.1 GI:17045484  
KEYWORDS  
human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Lillie, J., Brown, J.L., Bolt, A. and van Huffel, C.  
TITLE Novel genes, compositions and methods for the identification,  
assessment, prevention, and therapy of human cancers  
JOURNAL Patent: WO 0179556-A 601 25-OCT-2001;  
FEATURES  
Source 1..424  
Location/Qualifiers  
BASE COUNT 87 a 134 c 118 g 85 t  
ORIGIN  
Query Match 46.0%; Score 69; DB 6; Length 424;  
Best Local Similarity 88.2%; Pred. No. 8.2e-12;  
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
OY 51 GTGATCCCGCGGCTGCAGAAATTCGATATCAAGCTTATCGATACGCTGCAGCTGAGG 110  
DB 104 GTGATCCCGCGGCTGCAGAAATTCGATATCAAGCTTATCGATACGCTGCAGCTGAGG 45  
OY 111 GGGGGCTTAACCTAATTTTGT 135  
DB 44 GGGGGCGCGGTACCCAGCTTTTGT 20  
RESULT 13  
AY034154 2059 bp DNA circular SYN 23-JUL-2001  
LOCUS AY034154/c  
DEFINITION Cloning vector pIDN4, complete sequence.  
ACCESSION AY034154  
VERSION AY034154.1 GI:14324126



KEYWORDS  
SOURCE Cloning vector pIDN4.  
ORGANISM Cloning vector pIDN4.  
REFERENCE 1 (bases 1 to 2059)  
AUTHORS Hamilton,H.L., Schwartz,K.J. and Dillard,J.P.  
TITLE Insertion-duplication mutagenesis of neisseria: use in  
characterization of DNA transfer genes in the gonococcal genetic  
island  
JOURNAL J. Bacteriol. 183 (16), 4718-4726 (2001)  
MEDLINE 21359313  
PUBMED 11466274  
REFERENCE 2 (bases 1 to 2059)  
AUTHORS Hamilton,H.L., Schwartz,K.J. and Dillard,J.P.  
TITLE Direct Submision  
JOURNAL Submitted (11-MAY-2001) Medical Microbiology & Immunology,  
University of Wisconsin-Madison, 1300 University Avenue, Madison,  
WI 53706, USA  
FEATURES  
source Location/Qualifiers  
1. 2059  
/organism="Cloning vector pIDN4"  
/db\_xref="taxon:161273"  
/note="for insertion-duplication mutagenesis in Neisseria"  
40..59  
/note="T3"  
complement(187..204)  
/note="T7"  
277..311  
complement(310..1113)  
/gene="ermC"  
complement(310..1044)  
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EYFHPKPVYSSLDILNRKSRSHKDKOKYVFWKWKYKIKIFKQPNNSLKH  
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complement(1051..1054)  
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complement(1086..1091)  
/gene="ermC"  
complement(1108..1113)  
/gene="ermC"  
1130..1139  
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complement(1145..1154)  
/note="DNA uptake sequence (DUS)"  
complement(1276..11976)  
/note="RNA II"  
complement(1422..1423)  
1830..1835  
1854..1859  
1866..1873  
/note="RNA I"  
complement(1984..1989)  
complement(2007..2012)  
BASE COUNT 566 a 452 c 424 g 617 t  
ORIGIN  
Query Match 46.0%; Score 69; DB 12; Length 2059;  
Best Local Similarity 88.2%; Pred. No. 1.1e-11;  
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 51 GTGATCCCCCGGCTGAGGATTCGATCAAGCTTATGATACCGTGCAGCTCGAG 110  
DB 143 GTGATCCCCCGGCTGAGGATTCGATCAAGCTTATGATACCGTGCAGCTCGAG 110  
QY 111 GGGGCGCTACTACTATTGTT 135

Db 83 GGGGCGCGGTACCCAGCTTTGTT 59  
RESULT 14  
AB035274  
LOCUS  
DEFINITION Homo sapiens mRNA for postreplication repair protein hrad18p,  
complete cds.  
ACCESSION AB035274  
VERSION AB035274.1  
KEYWORDS GI:8980616.  
SOURCE Homo sapiens placenta CDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (sites)  
AUTHORS Tateishi,S., Sakuraba,Y., Masuyama,S., Inoue,H. and Yamazumi,M.  
TITLE Dysfunction of human Rad18 results in defective postreplication  
repair and hypersensitivity to multiple mutagens  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7927-7932 (2000)  
MEDLINE 20345089  
PUBMED  
REFERENCE 2 (bases 1 to 2890)  
AUTHORS Tateishi,S., Yamazumi,M. and Inoue,H.  
TITLE Direct Submision  
JOURNAL Submitted (26-NOV-1999) Satoshi Tateishi, Kumamoto University,  
Institute of Molecular Embryology; Kuhnouji 4-24-1, Kumamoto,  
Kumamoto 862-0976, Japan (E-mail:tateegpo.kumamoto-u.ac.jp,  
Tel:81-096-373-6602, Fax:81-096-373-6604)  
FEATURES  
source Location/Qualifiers  
1. 2890  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/chromosome="3"  
/tissue\_type="placenta"  
1..2890  
/gene="hrad18"  
126..1613  
/gene="hrad18"  
/note="RING-zinc-finger protein"  
/codon\_start=1  
/product="postreplication repair protein hrad18p"  
/protein\_id="BA99284.1"  
/db\_xref="GI:8980617"  
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YSCICIRKFLSYKTCPCVCTVTEPDILKNRITIDELIKYKSNRPNHLOFALSPAK  
KEASPAKTKKRRVETIAPDPSEKRRPEPSTSLKQVTVDPYGVNIPESHINK  
HIDSCISREKKEKESLRSSVHKRKLPLKTVYNLSDRLKRLKELGSLGIONKQOLIK  
RHQEVHMINACQDLAHPKSAEIVQETENIEKTRMLKELKESVAVFVKQDTEKE  
IDEIHSKYRKRRKSEFQLVQARKGYKRIAGMSOKYVITIKKEDESTEKLSYCMQGE  
DMWTSTVNTFSQSLDPELEPDEEDSSCIDIOEYLSSESDSCNSSSDIIRDL  
LEEBEAWASHKNDLQDTEISPRORRRRAESAEIERKRNKN"  
BASE COUNT 916 a 585 c 601 g 788 t  
ORIGIN  
Query Match 46.0%; Score 69; DB 9; Length 2890;  
Best Local Similarity 88.2%; Pred. No. 1.2e-11;  
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
QY 51 GTGATCCCCCGGCTGAGGATTCGATCAAGCTTATGATACCGTGCAGCTCGAG 110  
DB 2742 GTGATCCCCCGGCTGAGGATTCGATCAAGCTTATGATACCGTGCAGCTCGAG 2801  
QY 111 GGGGCGCTACTACTATTGTT 135  
DB 2802 GGGGCGCGGTACCCAGCTTTGTT 2826  
RESULT 15  
AX247548  
LOCUS  
DEFINITION Sequence 1 from Patent WO0166775.  
AX247548 2958 bp DNA linear PAT 28-SEP-2001

ACCESSION AX247548  
 VERSION AX247548.1 GI:15862240

KEYWORDS

SOURCE synthetic construct.  
 ORGANISM synthetic construct.  
 artificial sequences.

REFERENCE 1 (bases 1 to 2958)  
 AUTHORS Evans,D.H., Willer,D.O. and Yao,X.D.

TITLE Dna joining method  
 JOURNAL Patent: WO 0166775-A 1 13-SEP-2001;  
 University of Guelph (CA)

FEATURES  
 source location/Qualifiers

1..2958  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"

/note="pDW101"

BASE COUNT 748 a 735 c 752 g 723 t

ORIGIN

Query Match 46.0%; Score 69; DB 6; Length 2958;  
 Best Local Similarity 88.2%; Pred. No. 1.2e-11;

Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 51 GTGATCCCGCGGCTCGAGAAATCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110  
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 DB 684 GTGATCCCGCGGCTCGAGAAATCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 743

OY 111 GGGGCGCTAAGCTAATTTGTT 135  
 |||||||  
 DB 744 GGGGCGCGGTACCGAGCTTTGTT 768

Search completed: November 10, 2002, 06:53:07  
 Job time : 734.31 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:42:15 ; Search time 1350 Seconds

(without alignments)  
1799.499 Million cell updates/sec

Title: US-08-935-377-9

Perfect score: 150

Sequence: 1 GGCCAAATGTGAAACTA.....TTGTTTGTGGCCGCCGCC 150

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estb1:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estm:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_estc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: gb\_est6:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vit:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75.4	50.3	891	14	B0140386
2	73.2	48.8	807	17	CNS06CT6
3	72.2	48.1	728	10	AM682547
4	72	48.0	182	13	B1306115
5	72	48.0	793	14	B0143916
6	70.4	46.9	841	17	CNS06M11

C	7	70	46.7	682	17	A0074693	A0074693 CIT-HSP-2
C	8	69.8	46.5	361	17	CNS06CT6	AL392944 T7 end of
C	9	69.8	46.5	804	14	B0158468	B0158468 NF058H03P
C	10	69.4	46.3	182	13	B1305962	B1305962 NL-2_K23
C	11	69.4	46.3	186	13	B1305695	B1305695 NL-1_G23
C	12	69.4	46.3	742	17	CNS06V04	AL17458 T7 end of
C	13	69.2	46.1	912	17	CNS06UF5	AL145767 T7 end of
C	14	69	46.0	162	10	BE428068	BE428068 MTD002.H1
C	15	69	46.0	370	17	CNS06ME2	AL18320 T7 end of
C	16	69	46.0	300	9	AU234451	AU234451 AU234451
C	17	69	46.0	400	9	AU278852	AU278852 AU278852
C	18	69	46.0	864	17	A0937400	A0937400 NB2-011.H
C	19	68.8	45.9	175	13	B1306167	B1306167 NL-3_J08
C	20	68.8	45.9	182	13	B1306149	B1306149 NL-3_I07
C	21	68.8	45.9	182	13	B1306159	B1306159 NL-3_I22
C	22	68.8	45.9	182	13	B1306178	B1306178 NL-3_K05
C	23	68.8	45.9	182	13	B1306180	B1306180 NL-3_K07
C	24	68.8	45.9	757	14	B0155148	B0155148 NF076G11I
C	25	68.4	45.6	152	17	CNS06TR4	AL141902 T7 end of
C	26	68.2	45.5	312	13	BG919627	BG919627 602823186
C	27	68	45.3	295	10	BE428455	BE428455 MTD007.C0
C	28	68	45.3	608	17	A0009167	A0009167 CIT-HFP-2
C	29	68	45.3	907	17	CNS06VTP	AL1417037 T7 end of
C	30	67.6	45.1	157	17	CNS06VER	AL1416291 T7 end of
C	31	67.6	45.1	829	17	A0937397	A0937397 NB2-006.H
C	32	67.6	45.1	872	17	CNS06UB0	AL1415618 T7 end of
C	33	67.4	44.9	128	17	CNS07G34	AL1418916 T7 end of
C	34	67.4	44.9	528	17	B69688	AL1418916 T7 end of
C	35	67.4	44.9	802	17	CNS06WK6	AL1418916 T7 end of
C	36	67.4	44.9	901	17	CNS06WUM	AL1418916 T7 end of
C	37	67.2	44.8	240	17	CNS06V5T	AL1418916 T7 end of
C	38	67	44.7	107	13	BM398556	BM398556 5009-0-47
C	39	67	44.7	108	17	BE429251	BE429251 WHE0554.C
C	40	67	44.7	108	17	BE429251	BE429251 WHE0554.C
C	41	67	44.7	124	10	AW914179	AW914179 CIT-HSP-201
C	42	67	44.7	141	9	A0037147	A0037147 AU037147
C	43	67	44.7	141	17	B95279	B95279 CIT-HSP-217
C	44	67	44.7	144	17	B80294	B80294 CIT-HSP-204
C	45	67	44.7	157	12	BF281431	BF281431 EST446022

## ALIGNMENTS

RESULT 1  
LOCUS B0140386 891 bp mRNA linear EST 26-APR-2002  
DEFINITION NF035A10PH1081 Phoma-infected Medicago truncatula cDNA clone  
ACCESSION NF035A10PH 5', mRNA sequence.  
VERSION B0140386  
KEYWORDS B0140386.1 GI:20276512  
SOURCE EST.  
ORGANISM Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots;  
Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.

REFERENCE 1 (bases 1 to 891)  
AUTHORS Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,  
Gonzales,R.A., Bell,C.J., Inman,J.T., Naugh,M.E., Sullivan,J.P.,  
May,G.D. and Paiva,N.L.  
Expressed Sequence Tags from the Samuel Roberts Noble Foundation  
Medicago truncatula Phoma-infected library  
Unpublished (2002)  
CONTACT: Paiva NL  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7317  
Fax: 580 221 7380  
Email: nlpaiva@noble.org  
Insert length: 891 Std Error: 0.00

JOURNAL COMMENT

Plate: 035 row: A column: 10  
Seq primer: TCACACGAGAAACGCTATGAC.  
Location/Qualifiers  
1. .891

FEATURES  
SOURCE

/organism="Medicago truncatula"  
/db\_xref="taxon:3880"  
/clone="NF03A10PH"  
/clone\_1lb="Phoma-Infected"  
/tissue\_type="leaf"  
/dev\_stage="pathogen-induced, young trifoliolate"  
/note="Vector: pBluescript SK(-); Young trifoliolate leaves of Medicago truncatula were excised and dip-inoculated in a spore suspension of Phoma medicaginis, and inoculated in humid dishes. Pools of leaves were harvested at 0, 15, and 30 minutes and 1, 2, 3, 6, 14, 24, 48, 72, and 96, hours, and used to prepare total RNA. cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using Exasist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

BASE COUNT 188 a 131 c 64 g 224 t 264 others  
ORIGIN

Query Match 50.3%; Score 75.4; DB 14; Length 891;  
Best Local Similarity 87.8%; Pred. No. 1.3e-14;  
Matches 79; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 51 GTGATCCCGGGCTGCAGATTCGATATGATACCTGACCTCGAGG 110  
|||||  
Db 84 GTGATCCCGGGCTGCAGATTCGATATGATACCTGACCTCGAGG 143

OY 111 GGGGGCTACTACTAATTTTGTCTTGT 140  
|||||  
Db 144 GGGGGCCGCGTANCTAATTTTNTCTATWT 173

RESULT 2  
CNS06TYJ 807 bp DNA linear GSS 05-JUL-2001  
LOCUS  
DEFINITION  
of Pichia farinosa, genomic survey sequence.

ACCESSION  
AL415169  
VERSION  
AL415169.1  
KEYWORDS  
GSS.

SOURCE  
Pichia farinosa.

## ORGANISM

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; Saccharomycetaceae; Pichia.

REFERENCE  
AUTHORS

1 (bases 1 to 807)  
Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,  
Bollon-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S.,  
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,  
Malpertuy,A., Neuvéglise,C., Olier-Kalogeropoulos,O., Potier,S.,  
Saurin,W., Tekala,F., Toffano-Nicolas,C., Wesolowski-Louvel,M.,  
Wincker,P. and Weissenbach,J.  
Genomic exploration of the hemiascomycetous yeasts: 1. A set of  
yeast species for molecular evolution studies

## TITLE

JOURNAL  
MEDLINE  
PUBMED  
20584711

## JOURNAL

## MEDLINE

## PUBMED

## TITLE

JOURNAL  
MEDLINE  
PUBMED  
20584725

## JOURNAL

## MEDLINE

## PUBMED

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

## COMMENT

3 (bases 1 to 807)  
Genoscope.  
Direct Submission  
Submitted (07-SEP-2000) Genoscope - Centre National de Séquençage,  
2 rue Gaston Cremieux, CP 5706, 91057 Evry cedex, FRANCE. (E-mail :  
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
This GSS is part of a random genomic sequencing program of thirteen  
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces  
exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,  
Saccharomyces kluyveri, Kluyveromyces marxianus var. marxianus, Pichia  
lactis var. lactis, Kluyveromyces Hansenii, Pichia sorbitophila,  
angusta, Debaryomyces hansenii var. hansenii, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to  
5 kb were prepared and both extremities were sequenced. See  
keywords for description of this sequence and for the sequence of  
the other extremity of this insert.

FEATURES  
SOURCE

1. .807  
/organism="Pichia farinosa"  
/strain="CBS 7064"  
/db\_xref="taxon:4920"  
/clone="AX0AA003D05"  
/clone\_1lb="AX0AA"  
/note="end : 17"

BASE COUNT 230 a 186 c 125 g 218 t 48 others  
ORIGIN

Query Match 48.8%; Score 73.2; DB 17; Length 807;  
Best Local Similarity 79.1%; Pred. No. 7.1e-14;  
Matches 87; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

OY 8 AATTGAAAACGTAGATCTATTATTGACCGCGCCGACATACGTGATCCCGGCTG 67  
|||||  
Db 243 AATTGACCAATTGAGTTTTCATCGAAGAGATATTAACGCGATCCCGGCTG 302

OY 68 CAGGATTTGATATCAAGTTTCATACCGTCGACCTCGAGGGGGGCC 117  
|||||  
Db 303 CAGGAATTCGATATCAAGTTTCATACCGTCGACCTCGAGGGGGGCC 352

RESULT 3  
AM682547/C 728 bp mRNA linear EST 14-APR-2000  
LOCUS  
DEFINITION  
EST01410 E8.5 mouse craniofacial subtraction cDNA library Mus  
musculus cDNA clone e064, mRNA sequence.

ACCESSION  
AM682547  
VERSION  
AM682547.1  
KEYWORDS  
EST.

SOURCE  
house mouse.  
ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 728)  
Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
EST sequences from E8.5 mouse craniofacial cDNA library

Unpublished (2000)  
Contact: Yoshihiko Yamada  
Craniofacial Developmental Biology and Regeneration Branch  
National Institute of Dental and Craniofacial Research  
9000 Rockville Pike, Building 30, Room 405, NIDCR, NIH, Bethesda,  
MD 20892

Tel: 301 496 2111  
Fax: 301 402 0897  
Email: yoshi.yamada@nih.gov  
Seq primer: M13 reverse.  
Location/Qualifiers  
1. .728

/organism="Mus musculus"  
/strain="ICR"  
/db\_xref="taxon:10090"  
/clone="e064"  
/clone\_1lb="E8.5 mouse craniofacial subtraction cDNA  
library"

FEATURES  
SOURCE

111 GGGGCTACTAAT 130

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetaceae; Saccharomyces

REFERENCE 1 (bases 1 to 841)  
 AUTHORS Souciet,J., Aigle,M., Artiguenave,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neveuglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekai,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Winkler,P. and Weissbach,J.  
 TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies  
 JOURNAL MEDLINE 20584711  
 PUBMED 11152876  
 REFERENCE 2 (bases 1 to 841)  
 AUTHORS de Montigny,J., Spehner,C., Souciet,J., Tekai,F., Dujon,B., Winkler,P., Artiguenave,F. and Potier,S.  
 COMMENT Genomic exploration of the hemiascomycetous yeasts: 15. *Pichia sorbitophila*  
 JOURNAL FEBS Lett. 487 (1), 87-90 (2000)  
 MEDLINE 20584725  
 PUBMED 11152890  
 REFERENCE 3 (bases 1 to 841)  
 AUTHORS Direct Submission  
 TITLE Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Creneau, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: segre@genoscope.cns.fr - Web: www.genoscope.cns.fr)  
 COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvurum*, *Saccharomyces exiguus*, *Saccharomyces servazii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbitophila*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.  
 FEATURES  
 source Location/Qualifiers  
 1. 841  
 /organism="Pichia farinosa"  
 /db\_xref="taxon:4920"  
 /clone="AX0A027B04"  
 /clone\_lib="AX0A"  
 /note="end: 17"  
 BASE COUNT 238 a 174 c 246 g 182 t 1 others  
 ORIGIN  
 Query Match 46.9%; Score 70.4; DB 17; Length 841;  
 Best Local Similarity 98.6%; Pred. No. 6.2e-13;  
 Matches 71; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 46 ATGACGTGATCCCCGGGCTGAGAAATTCGATATCAGCTTATCGATACCGTCGACT 105  
 Db 744 ATGACGAGAGATCCCCGGGCTGCGAGAAITTCGATATCAGCTTATCGATACCGTCGACT 803  
 QY 106 CGAGGGGGGGGCC 117  
 Db 804 CGAGGGGGGGGCC 815  
 RESULT 7  
 LOCUS A0074693/c 682 bp DNA linear GSS 20-AUG-1998  
 DEFINITION CIT-HSP-2301L23.TF CIT-HSP Homo sapiens genomic clone 2301L23. DNA sequence.  
 ACCESSION A0074693  
 VERSION A0074693.1 GI:3436811  
 KEYWORDS GSS.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 682)

AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.  
 TITLE Use of a random human BAC End Sequence Database for Sequence-Ready Map Building  
 JOURNAL Unpublished (1998)  
 COMMENT Contact: Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: mdadams@ligr.org  
 Clones are available from Research Genetics (info@resgen.com). BAC end search page:  
 http://www.tigr.org/tldb/humgen/bac\_end\_search/bac\_end\_search.html.  
 Seq primer: M13-21  
 Class: BAC ends.  
 FEATURES  
 source Location/Qualifiers  
 1. 682  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="2301L23"  
 /clone\_lib="CIT-HSP"  
 /sex="Male"  
 /cell\_type="Sperm"  
 /note="Vector: pBelBAC11; Site.1: HindIII; Site.2: HindIII"  
 BASE COUNT 156 a 187 c 187 g 151 t 1 others  
 ORIGIN  
 Query Match 46.7%; Score 70; DB 17; Length 682;  
 Best Local Similarity 93.6%; Pred. No. 8.4e-13;  
 Matches 73; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 51 GTGGATCCCCGGGCTGAGAAATTCGATATCAGCTTATCGATACCGTCGAGG 110  
 Db 78 GTGGATCCCCGGGCTGCGAGAAITTCGATATCAGCTTATCGATACCGTCGAGG 19  
 QY 111 GGGGGCTTACTTACTAA 128  
 Db 18 GGGGGCGCCGAGTACCAA 1  
 RESULT 8  
 LOCUS CNS06CT6 361 bp DNA linear GSS 05-APR-2001  
 DEFINITION T7 end of clone AR0A007H05 of library AR0A from strain CBS 732 of *Zygosaccharomyces rouxii*, genomic survey sequence.  
 ACCESSION AL392944.1 GI:12142764  
 VERSION AL392944.1  
 KEYWORDS GSS; clone AR0A007H05; RST AR0A007H05CPL.  
 SOURCE *Zygosaccharomyces rouxii*.  
 ORGANISM *Zygosaccharomyces rouxii*.  
 Eukaryota; Fungi; Ascomycota; *Saccharomycotina*; *Saccharomycetes*; *Saccharomycetales*; *Saccharomycetaceae*; *Zygosaccharomyces*.  
 REFERENCE 1 (bases 1 to 361)  
 AUTHORS Souciet,J., Aigle,M., Artiguenave,F., Blandin,G., Bolotin-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S., de-Montigny,J., Dujon,B., Durens,P., Lepingle,A., Llorente,B., Malpertuy,A., Neveuglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekai,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Winkler,P. and Weissbach,J.  
 TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies  
 JOURNAL MEDLINE 20584711  
 PUBMED 11152876  
 REFERENCE 2 (bases 1 to 361)  
 AUTHORS de Montigny,J., Straub,M., Potier,S., Tekai,F., Dujon,B., Winkler,P., Artiguenave,F. and Souciet,J.  
 COMMENT Genomic exploration of the hemiascomycetous yeasts: 8. *Zygosaccharomyces rouxii*

[illegible]

FEATURES	source
<p>The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7325 Fax: 580 221 7380 Email: <a href="mailto:mjharlison@noble.org">mjharlison@noble.org</a> Insert Length: 804 Std Error: 0.00 Plate: 058 row: H column: 09 Seq primer: TCACACAGGAACAGCATATGAC.</p>	
FEATURES	source
<p>1. 804 /organism="Medicago truncatula" /db_xref="taxon:3880" /clone="NF058H09PL" /clone.lib="Phosphate starved leaf" /tissue.type="leaf" /dev_stage="trifoliolate" /note="Vector: Lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20uM potassium phosphate. RNA was prepared from above ground tissues."</p>	
BASE COUNT	215 a 202 c 181 g 165 t 41 others
ORIGIN	
Query Match	46.5%; Score 69.8; DB 14; Length 804;
Best Local Similarity	89.2%; Pred. No. 9,9e-13;
Matches 74; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	
OY 51 GTGATGCCCCGGGGCGCGAATTCGATTCATCAGCTTATCGATACCGTCGACCTGAGG 110	
Db 82 GTGATGCCCCGGGGCTGCGAGATTCGATACCAAGCTTATGATACCGTCGACCTGAGG 141	
OY 111 GGGGGCCCTACATCACTAATTTTG 133	
Db 142 GGGGGCCCTGATCAACCAATTTG 164	
RESULT 10	
BI305962/c	182 bp mRNA linear EST 20-JUL-2001
LOCUS	BI305962
DEFINITION	NL_2_K23 Drought stress (leaf) Oryza sativa cDNA clone NL_2_K23 3', mRNA sequence.
ACCESSION	BI305962
VERSION	BI305962.1 GI:14981284
KEYWORDS	EST.
SOURCE	Oryza sativa.
ORGANISM	Oryza sativa.
REFERENCE	Eukaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta; Euphorbiata: Magnoliophyta: Liliopsida; Poales; Poaceae; Ehrhacridae; Oryzaceae; Oryza.
AUTHORS	1 (bases 1 to 182) Reddy,A.R., Ramakrishna,W., Chandrasekhar,A., Nagabushan,I., Ravindrababu,P. and Bennetzen,J.L.
TITLE	Novel EST enrichment with normalized cDNA libraries from drought stressed rice (Oryza sativa L.cv Nagina 22)
JOURNAL	Unpublished (2001)
COMMENT	Contact: Reddy AR Department of Plant Sciences, School of Life Sciences University of Hyderabad P.O. Central University, Hyderabad-500 046, A.P, India Tel. 0091-40-3010265 Fax: 0091-40-3010145 Email: arjulsleu@uhyd.ernet.in Insert Length: 182 Std Error: 0.00 Plate: 2 row: K column: 23 Seq primer: GTAAACGACGGCCATGG.
FEATURES	source
<p>1. 182 /organism="Oryza sativa" /cultivar="Nagina 22 (indica sub sp)" /db_xref="taxon:4530" /clone="NL_2_K23"</p>	

/clone.lib="Drought stress (leaf)"  
 /tissue\_type="Entire leaf tissue"  
 /dev\_stage="35 day-old seedlings"  
 /note="Organ: Leaf; Vector: T7T3Pac; ESTs from normalized  
 leaf cDNA library from drought stressed seedlings"

BASE COUNT 34 a 48 c 52 g 46 t 2 others

Query Match 46.3%; Score 69.4; DB 13; Length 182;  
 Best Local Similarity 91.2%; Pred. No. 1.3e-12;  
 Matches 73; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 51 GTGATCCCGGGGCTGAGATTCGATTCAGCTTATCGATACCGTCGACCTGAGG 110  
 |||||  
 Db 107 GTGATCCCGGGGCTGAGATTCGATTCAGCTTATCGATACCGTCGACCTGAGG 48

OY 111 GGGGGCTTAACCTAATT 130  
 |||||  
 Db 47 GGGGGCNCGGTACCAATT 28

RESULT 11  
 BI305695/c 186 bp mRNA linear EST 20-JUL-2001  
 LOCUS NL\_1.G23 Drought stress (leaf) Oryza sativa cDNA clone NL\_1.G23 3',  
 DEFINITION mRNA sequence.  
 ACCESSION BI305695  
 VERSION BI305695.1 GI:14981017  
 KEYWORDS EST.  
 SOURCE Oryza sativa.  
 ORGANISM Oryza sativa

REFERENCE  
 AUTHORS Reddy,A.R., Kamakrishna,W., Chandrasekhar,A., Nagabhushan,I.,  
 Ravindrababu,P. and Bennetzen,J.L.  
 TITLE Novel EST enrichment with normalized cDNA libraries from drought  
 stressed rice (Oryza sativa L.cv Nagina 22)  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Reddy AR

Department of Plant Sciences, School of Life Sciences  
 University of Hyderabad  
 P.O. Central University, Hyderabad-500 046, A.P, India  
 Tel: 0091-40-3010265  
 Fax: 0091-40-3010145  
 Email: arjulsleubhd.ernet.in  
 Insert Length: 186 Std Error: 0.00  
 Plate: 1 row: 6 column: 23  
 Seq primer: GTAAACGAGCGCCAGTG.  
 Location/Qualifiers

FEATURES  
 source 1..186  
 /organism="Oryza sativa"  
 /cultivar="Nagina 22 (Indica sub sp)"  
 /db\_xref="taxon:4530"  
 /clone="NL\_1.G23"  
 /clone.lib="Drought stress (leaf)"  
 /tissue\_type="Entire leaf tissue"  
 /dev\_stage="35 day-old seedlings"  
 /note="Organ: Leaf; Vector: T7T3Pac; ESTs from normalized  
 leaf cDNA library from drought stressed seedlings"

BASE COUNT 35 a 47 c 56 g 46 t 2 others

Query Match 46.3%; Score 69.4; DB 13; Length 186;  
 Best Local Similarity 91.2%; Pred. No. 1.3e-12;  
 Matches 73; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 51 GTGATCCCGGGGCTGAGATTCGATTCAGCTTATCGATACCGTCGACCTGAGG 110  
 |||||  
 Db 111 GTGATCCCGGGGCTGAGATTCGATTCAGCTTATCGATACCGTCGACCTGAGG 52  
 OY 111 GGGGGCTTAACCTAATT 130

Db 51 GGGGGCNCGGTACCAATT 32  
 |||||

RESULT 12  
 CNS06V04 742 bp DNA linear GSS 06-JUL-2001  
 LOCUS T7 end of clone AX0A024B10 of library AX0A from strain CBS 7064  
 DEFINITION of Pichia farinosa, genomic survey sequence.  
 AL117458  
 AL117458.1 GI:12199166  
 GSS.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Pichia farinosa.  
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 Saccharomycetales; Saccharomycetaceae; Pichia.

REFERENCE  
 AUTHORS Soucier,J.L., Aigle,M., Attiguenave,F., Blandin,G.,  
 Soucier,J.L., Aigle,M., Attiguenave,F., Blandin,G.,  
 Bolotin-Fukuhara,M., Bon,E., Brotier,P., Casaregola,S.,  
 de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,  
 Malpertuy,A., Neugeglise,C., Ozier-Kalogeropoulou,O., Potier,S.,  
 Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,  
 Wincker,P. and Weissenbach,J.

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 AUTHORS

2 (bases 1 to 742)  
 de Montigny,J., Spehner,C., Soucier,J., Tekala,F., Dujon,B.,  
 Wincker,P., Attiguenave,F. and Potier,S.  
 Genomic exploration of the hemiascomycetous yeasts: 15. Pichia  
 sorbitophila  
 FEBS Lett. 487 (1), 87-90 (2000)  
 11152876  
 20584711  
 11152876  
 2 (bases 1 to 742)  
 de Montigny,J., Spehner,C., Soucier,J., Tekala,F., Dujon,B.,  
 Wincker,P., Attiguenave,F. and Potier,S.  
 Genomic exploration of the hemiascomycetous yeasts: 15. Pichia  
 sorbitophila  
 FEBS Lett. 487 (1), 87-90 (2000)  
 11152876  
 20584711  
 11152876  
 3 (bases 1 to 742)  
 Genoscope.  
 Direct Submission  
 Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,  
 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :  
 seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT  
 This GSS is part of a random genomic sequencing program of thirteen  
 yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces  
 exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,  
 Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces  
 lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia  
 angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,  
 Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to  
 5 kb were prepared and both extremities were sequenced. See  
 keywords for description of this sequence and for the sequence of  
 the other extremity of this insert.  
 Location/Qualifiers

FEATURES  
 source 1..742  
 /organism="Pichia farinosa"  
 /strain="CBS 7064"  
 /db\_xref="taxon:4920"  
 /clone="AX0A024B10"  
 /clone.lib="AX0A"  
 /note="end : 77"  
 complement(<3..>641)  
 /note="similar to Saccharomyces cerevisiae ORF YDR238c [SEC26 : coatomer complex beta chain of secretory pathway  
 vesicles]"

BASE COUNT 207 a 154 c 156 g 224 t 1 others

Query Match 46.3%; Score 69.4; DB 17; Length 742;  
 Best Local Similarity 83.2%; Pred. No. 1.3e-12;  
 Matches 79; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 23 TCTATTATTGACGCGCGCCGATGATGATCCCGGGCTGAGATTCGATTC 82



```

Db      614  TCAATTTACCGCTGTTGTCACCTGAGGAGATCCCGGGCTGCAGGAATTCGATATC 673
QY      83  AAGCTTATCGATACCGTCGACCTCGAGGGGGAGGCC 117
Db      674  AAGCTTATCGATACCGTCGACCTCGAGGGGGAGGCC 708

RESULT 13
CNS06UF5
LOCUS   912 bp    DNA    linear    GSS 06-JUL-2001
DEFINITION T7 end of clone AX0AA008E09 of library AX0A from strain CBS 7064
ACCESSION AL415767
VERSION   AL415767.1  GI:12195405
KEYWORDS  GSS.
SOURCE    Pichia farinosa.
ORGANISM  Pichia farinosa
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
REFERENCE 1 (bases 1 to 912)
AUTHORS   Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
deMontigny,J., Dujon,B., Durrens,P., Lepoint,A., Llorente,B.,
Malpertuy,A., Neuvéglise,C., Olier-Kaiogopoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Mincker,P. and Weissenbach,J.
TITLE      Genomic exploration of the hemiascomycetous yeasts: 1. A set of
JOURNAL    yeast species for molecular evolution studies
MEDLINE    FEBS Lett. 487 (1), 3-12 (2000)
PUBMED     20584711
11152876
2 (bases 1 to 912)
de Montigny,J., Spehner,C., Souciet,J., Tekala,F., Dujon,B.,
Mincker,P., Artiguenave,F. and Potier,S.
TITLE      Genomic exploration of the hemiascomycetous yeasts: 15. Pichia
JOURNAL    Sorbitophila
MEDLINE    FEBS Lett. 487 (1), 87-90 (2000)
PUBMED     20584725
11152890
3 (bases 1 to 912)
Genoscope.
REFERENCE 3
AUTHORS   Submitted (07-SEP-2000) Genoscope - Centre National de Séquençage,
JOURNAL    2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT    This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces servazii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces marxianus var. marxianus, Pichia
lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
the other extremity of this insert.
FEATURES
source
1..912
/organism="Pichia farinosa"
/strain="CBS 7064"
/db_xref="taxon:4920"
/clone="AX0AA008E09"
/clone_1id="AX0AA"
/note="end : T7"
BASE COUNT 298 a 210 c 160 g 240 t 4 others
ORIGIN
Query Match 46.1%; Score 69.2; DB 17; Length 912;
Best Local Similarity 88.1%; Pred. No. 1.6e-12;
Matches 74; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 52 TGGATCCCCCGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 111
|||||

```

```

Db      817  TGGATCCCCCGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 876
QY      112  GGGGCTACTACTACTACTATTTTGT 135
Db      877  GGGGGCCCGGTACACGACTTTTGT 900

RESULT 14
BE428068
LOCUS   162 bp    mRNA    linear    EST 26-JUL-2000
DEFINITION MTD002.H10F990615 ITFC MTD Durum wheat Root Library Triticum
turgidum subsp. durum cDNA clone MTD002.H10, mRNA sequence.
ACCESSION BE428068
VERSION   BE428068.1  GI:9425911
KEYWORDS  EST.
SOURCE    durum wheat.
ORGANISM  Triticum turgidum subsp. durum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 162)
AUTHORS   Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,
Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,
Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,
Pechioni,N., Qualset,C., Schuch,W., Selvaraj,G., Sharifou,M.,
Sorelli,M., Warburton,M. and Wenzel,G.
TITLE      International Triticace EST Cooperative (ITEC): Production of
JOURNAL    Expressed Sequence Tags for Species of the Triticeae
MEDLINE    Unpublished (2000)
PUBMED
COMMENT    Contact: Joudrier P
INRA, Unite de Biochimie et Biologie Moléculaire des Cereales
2, place VIALA, 34060 Montpellier cedex 01 FRANCE
Tel: 33 4 99 61 23 84
Fax: 33 4 99 61 23 48
Email: joudrier@enscm.inra.fr
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
FEATURES
source
1..162
/organism="Triticum turgidum subsp. durum"
/cultivar="Siliana"
/db_xref="taxon:4567"
/clone="MTD002.H10"
/clone_1id="ITEC MTD Durum Wheat Root Library"
/tissue_type="root"
/dev_stage="3-day-old seedling, water-stressed"
/note="Vector: pSPORT1, T7 primers used. See pSPORT1
polylinker site. 0.3-2.0 kbp average insert size."
BASE COUNT 28 a 42 c 49 g 43 t
ORIGIN
Query Match 46.0%; Score 69; DB 10; Length 162;
Best Local Similarity 88.2%; Pred. No. 1.7e-12;
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 51 GTGATCCCCCGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
|||||
Db 24 GTGGATCCCCCGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 83
QY 111 GGGGGCTACTACTACTATTTTGT 135
|||||
Db 84 GGGGGCCCGGTACACGACTTTTGT 108
|||||

RESULT 15
CNS06WE2
LOCUS   370 bp    DNA    linear    GSS 06-JUL-2001
DEFINITION T7 end of clone AX0AA030G01 of library AX0A from strain CBS 7064
ACCESSION AL418320
VERSION   AL418320.1  GI:12200918
KEYWORDS  GSS.

```



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 04:19:15 ; Search time 176.987 Seconds

(without alignments)  
1908.619 Million cell updates/sec

Title: US-08-935-377-9

150

Perfect score: 1 GGCCAAATTTGAAAACTA.....TTGTTTGTGGCCCGGCC 150

Sequence:

Scoring table:

IDENTITY\_NUC

Gap 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: N.Geneseq\_101002.\*  
2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.\*  
3: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*  
4: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*  
5: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*  
6: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.\*  
7: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.\*  
8: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.\*  
9: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.\*  
10: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.\*  
11: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.\*  
12: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.\*  
13: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.\*  
14: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.\*  
15: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.\*  
16: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.\*  
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19: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.\*  
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21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.\*  
22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*  
23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*  
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	150	100.0	150	21	AAA15238
2	150	100.0	150	22	ABA01479
3	150	100.0	150	24	AA031781
4	138	92.0	149	21	AAA15237
5	138	92.0	149	22	ABA01478
6	138	92.0	149	24	AA031780
7	136	90.7	148	21	AAA15236
8	136	90.7	148	22	ABA01477
9	136	90.7	148	24	AA031779

10	130	86.7	145	21	AAA15235	Nucleotide sequenc
11	130	86.7	145	22	ABA01476	Partial p7.5/ATG3/
12	130	86.7	145	24	AA031778	Modified p7.5/ck v
13	75	50.0	611	23	ABV42990	Human prostate exp
14	74.8	49.9	432	23	ABV38237	Human prostate exp
15	74.4	49.6	508	23	ABV39281	Human prostate exp
16	74.2	49.5	528	23	ABV38626	Human prostate exp
17	74	49.3	612	23	ABV34128	Human prostate exp
18	73.4	48.9	450	23	ABV38398	Human prostate exp
19	73.4	48.9	467	23	ABV45888	Human prostate exp
20	73.4	48.9	573	23	ABV38615	Human prostate exp
21	73	48.7	410	23	ABV38443	Human prostate exp
22	72.2	48.1	684	23	ABV36344	Human prostate exp
23	72.2	48.1	855	24	ABV45375	Human prostate exp
24	72.2	48.1	855	24	ABV60152	Human prostate exp
25	72	48.0	276	23	ABV35118	Fungi stress respo
26	71.8	47.9	372	23	ABV43508	Human prostate exp
27	71.8	47.9	393	23	ABV36203	Human prostate exp
28	71.8	47.9	393	23	ABV45252	Human prostate exp
29	71.8	47.9	408	23	ABV35567	Human prostate exp
30	71.8	47.9	416	23	ABV38388	Human prostate exp
31	71.8	47.9	417	23	ABV42673	Human prostate exp
32	71.8	47.9	465	23	ABV35114	Human prostate exp
33	71.8	47.9	466	23	ABV35226	Human prostate exp
34	71.8	47.9	469	23	ABV42812	Human prostate exp
35	71.8	47.9	474	23	ABV34198	Human prostate exp
36	71.8	47.9	474	23	ABV43059	Human prostate exp
37	71.8	47.9	565	23	ABV34124	Human prostate exp
38	71.8	47.9	565	23	ABV42986	Human prostate exp
39	71.8	47.9	615	23	ABV38816	Human prostate exp
40	71.8	47.9	619	23	ABV32153	Human prostate exp
41	71.6	47.7	460	23	ABV33323	Human prostate exp
42	71.6	47.7	460	23	ABV42246	Human prostate exp
43	71.4	47.6	410	23	ABV32098	Human prostate exp
44	71.4	47.6	410	23	ABV41036	Human prostate exp
45	71.4	47.6	426	23	ABV38236	Human prostate exp

#### ALIGNMENTS

RESULT 1	
AAA15238	
ID	AAA15238 standard; DNA; 150 BP.
XX	
AC	AAA15238;
XX	
DT	04-SEP-2000 (first entry)
XX	
DE	Nucleotide sequence of a fragment of the plasmid p7.5/ATG3/ck.
XX	
KW	Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen.
KW	vaccine; tumour regression; cancer; infection; ss.
XX	
OS	Synthetic.
XX	
PN	WO200028016-A1.
XX	
PD	18-MAY-2000.
XX	
PF	10-NOV-1998; 98WO-US24029.
XX	
PR	10-NOV-1998; 98WO-US24029.
XX	
PA	(UTRP) UNITV ROCHESTER.
XX	
PI	Zauderer M;
XX	
DR	WPI; 2000-376533/32.
XX	
PT	Novel method of identifying target epitopes or antigens specific for
PT	human tumors, cancers and infected cells involving screening expression
PT	library products of a cell expressing the target epitope





```

XX Cell death; toxic gene; tumour suppressor; ds.
XX Synthetic.
XX WO200172995-A2.
XX 04-OCT-2001.
XX 28-MAR-2001; 2001WO-US09953.
XX 28-MAR-2000; 2000US-0192586.
XX 10-MAY-2000; 2000US-0203343.
XX 23-JAN-2001; 2001US-0263226.
XX 27-FEB-2001; 2001US-0271426.
XX (UNRP ) UNIV ROCHESTER.
XX Zauderer M, Smith ES;
XX WPI; 2001-570897/64.
XX Selecting target polynucleotides, particularly toxic genes, involves
XX introducing a library of insert polynucleotides into a host cell
XX population, where the target polynucleotide promotes cell death -
XX Disclosure; Fig 8; 359pp; English.
XX The present invention relates to a method for selecting a target
XX polynucleotide. The method comprises introducing into a host cell
XX a population a library of insert polynucleotides, where expression of the
XX target polynucleotide directly or indirectly promotes host cell death.
XX The cells are cultured and the insert polynucleotides are collected from
XX the cells which die. The method is useful for selecting target
XX polynucleotides, particularly polynucleotides which alter cell phenotypes
XX of induce or inhibit cell death. The method can be used to isolate toxic
XX genes such as tumour suppressors. The present sequence was used to
XX illustrate the method of the the present invention.
XX Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;
XX SQ
XX Query Match 92.0%; Score 138; DB 22; Length 149;
XX Best Local Similarity 99.3%; Pred. No. 1.7e-38;
XX Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GCCCAAAATTTGAAAACCTAGATCTATTATTCGACGGCGCCGCAATGACGTGATCCCC 60
DB 1 GGGCAAAAATTTGAAAACCTAGATCTATTATTCGACGGCGCCGCAATGA-GTGGATCCCC 59
QY 61 CGGCGTCGAGGAATTCGATTCAGATTCAGTACCGTCGACCTCGAGGGGGGCGCTTAA 120
DB 60 CGGGCTCGAGGAATTCGATTCAGATTCAGTACCGTCGACCTCGAGGGGGGCGCTTAA 119
QY 121 CTAACCTAATTTGTTTGTGTGGGGCCGCC 150
DB 120 CTAACCTAATTTGTTTGTGTGGGGCCGCC 149

```

RESULT 6  
AAD31780  
ID AAD31780 standard; DNA; 149 BP.

AC AAD31780;  
XX 18-JUN-2002 (first entry)  
XX Modified p7.5/tk vector, p7.5/ATG2/tk.  
XX Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;  
XX vaccine; immune response; cytosolic; p7.5/tk vector; thymidine kinase;  
XX p7.5/ATG2/tk vector; ds.  
XX Vaccinia virus.

```

OS Synthetic.
XX Key Location/Qualifiers
XX misc_signal 46..48
XX /*tag= a
XX /*note= "translation start codon"
XX 117..119
XX /*tag= b
XX /*note= "translation stop codon"
XX 121..123
XX /*tag= c
XX /*note= "translation stop codon"
XX 125..127
XX /*tag= d
XX /*note= "translation stop codon"
XX 133..139
XX /*tag= e
XX /*note= "transcription stop signal"
XX US2002018785-A1.
XX 14-FEB-2002.
XX 02-APR-2001; 2001US-0822250.
XX 22-SEP-1997; 97US-0935377.
XX (UNRP ) UNIV ROCHESTER.
XX Zauderer M;
XX WPI; 2002-239252/29.
XX Representational Difference Analysis method for identification of
XX antigens recognized by cytotoxic T cells and specific for human tumors,
XX comprises improved selection of genes encoding target antigens
XX Example 1; Fig 2; 54pp; English.
XX The present invention relates to novel methods for the identification
XX of antigens recognised by cytotoxic T cells (CTLs) and specific for
XX human tumours, cancers and infected cells. The method involves screening
XX the products of an expression library generated from DNA/RNA of a cell
XX expressing a target epitope with cytotoxic T cells generated against
XX the cell to identify DNA clones expressing target epitope or providing
XX cytotoxic T cells specific for a gene product differentially expressed
XX by a cell and measuring the cross-reactivity of the cytotoxic T cells
XX for cells expressing a target epitope in which the target epitope is
XX identified as a gene product inducing cytotoxic T cells. The method is
XX useful for identifying a target epitope or antigen specific for a tumour
XX cell. The target epitope is also useful for identifying target antigens
XX against the tumour cells against which it is desirable to induce cell-
XX mediated immunity. The antigen identified by the method is useful
XX in immunogenic compositions and vaccine preparations to induce the
XX regression of tumours, cancers and infections in mammals. The invention
XX also relates to vaccinia viral vectors which are useful for treating
XX tumour-bearing mammals, including humans to generate immune response
XX against the tumour cells. They are also useful for immunising or
XX vaccinating tumour-free subjects to prevent tumour formation. The
XX present sequence is modified p7.5/tk (thymidine kinase) vector,
XX p7.5/ATG2/tk. This vector comprises a vaccinia virus 7.5k promoter and
XX a modified tk DNA fragment. This vector is used in the exemplification
XX of the invention.
XX Sequence 149 BP; 36 A; 37 C; 39 G; 37 T; 0 other;
XX SQ
XX Query Match 92.0%; Score 138; DB 24; Length 149;
XX Best Local Similarity 99.3%; Pred. No. 1.7e-38;
XX Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GCCCAAAATTTGAAAACCTAGATCTATTATTCGACGGCGCCGCAATGACGTGATCCCC 60
DB 1 GGGCAAAAATTTGAAAACCTAGATCTATTATTCGACGGCGCCGCAATGA-GTGGATCCCC 59

```

QY 61 CGGGCTCAGGAATTCGATATCAAGCTTATCGATACCTCGACCTCGAGGGGGGCTTAA 120  
|  
Db 60 CGGGCTCAGGAATTCGATATCAAGCTTATCGATACCTCGAGGGGGGCTTAA 119  
QY 121 CTAACTAATTTTGTGTTTGTGGCCCGGCC 150  
|  
Db 120 CTAACTAATTTTGTGTTTGTGGCCCGGCC 149

RESULT 7  
AAAI5236  
ID AAI5236 standard; DNA; 148 BP.  
XX  
AC AAI5236;  
XX  
DT 04-SEP-2000 (first entry)  
XX  
DE Nucleotide sequence of a fragment of the plasmid p7.5/ATG1/tk.  
XX  
KM Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;  
XX vaccine; tumour regression; cancer; infection; ss.  
OS Synthetic.  
XX  
PN WO200028016-A1.  
PD 18-MAY-2000.  
XX  
PF 10-NOV-1998; 98WO-US24029.  
XX  
PR 10-NOV-1998; 98WO-US24029.  
XX  
PA (UVRP ) UNIV ROCHESTER.  
XX  
PI Zauderer M;  
XX  
DR WPI: 2000-376533/32.

Novel method of identifying target epitopes or antigens specific for human tumors, cancers and infected cells involving screening expression library products of a cell expressing the target epitope -

Disclosure: Fig 2; 132pp; English.

The present sequence represents a fragment of a vaccinia transfer plasmid, which is used in the course of the invention. The specification describes a method for identifying a target epitope. The method comprises screening the products of an expression library from a cell expressing the target epitope with cytotoxic T cells generated against the cell to identify DNA clones expressing the target epitope. The method may also comprise providing a cytotoxic T cell specific for a gene product differentially expressed by a cell and measuring the cross-reactivity of the cytotoxic T cell. The methods are useful for identifying tumour specific target epitopes and antigens which are useful in immunogenic compositions or vaccines to induce the regression of tumors, cancers or infections in mammals. The genes expressed in a panel of tumour cells that are derived from single immortalised, non-tumorigenic cell line are used to generate HLA restricted cytotoxic T cells which are evaluated for activity against tumour cells. The method is useful to identify potential antigens expressed not only by the pathogen but also by the host cells whose gene expression is altered as a result of infection. The differential gene expression strategies can be applied to identify immunogenic molecules of cells infected with virus, fungus or mycobacterium.

Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;

Query Match 90.7%; Score 136; DB 21; Length 148;  
Best Local Similarity 98.7%; Pred. No. 8,4e-38;  
Matches 148; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 GGCCAAAATTTGAAAACTAGATCTATTATTGACGCGCGCCCATGACGTGATCCCC 60

Db 1 GGCCAAAATTTGAAAACTAGATCTATTATTGACGCGCGCCCATG--GTGGATCCCC 58  
|  
QY 61 CGGGCTCAGGAATTCGATATCAAGCTTATCGATACCTCGAGGGGGGCTTAA 120  
|  
Db 59 CGGGCTCAGGAATTCGATATCAAGCTTATCGATACCTCGAGGGGGGCTTAA 118  
QY 121 CTAACTAATTTTGTGTTTGTGGCCCGGCC 150  
|  
Db 119 CTAACTAATTTTGTGTTTGTGGCCCGGCC 148

RESULT 8  
ABA01477  
ID ABA01477 standard; DNA; 148 BP.  
XX  
AC ABA01477;  
XX  
DT 04-FEB-2002 (first entry)  
XX  
DE Partial p7.5/ATG1/tk sequence.  
XX  
KM Cell death; toxic gene; tumour suppressor; ds.  
XX  
OS Synthetic.  
XX  
PN WO200172995-A2.  
PD 04-OCT-2001.  
XX  
PF 28-MAR-2001; 2001WO-US09953.  
XX  
PR 28-MAR-2000; 2000US-0192586.  
XX  
PR 10-MAY-2000; 2000US-0203343.  
XX  
PR 23-JAN-2001; 2001US-0263226.  
XX  
PR 27-FEB-2001; 2001US-0271426.  
XX  
PA (UVRP ) UNIV ROCHESTER.  
XX  
PI Zauderer M, Smith ES;  
XX  
DR WPI: 2001-570897/64.

Selecting target polynucleotides, particularly toxic genes, involves introducing a library of insert polynucleotides into a host cell population, where the target polynucleotide promotes cell death -

Disclosure: Fig 8; 359pp; English.

The present invention relates to a method for selecting a target polynucleotide. The method comprises introducing into a host cell population a library of insert polynucleotides, where expression of the target polynucleotide directly or indirectly promotes host cell death. The cells are cultured and the insert polynucleotides are collected from the cells which die. The method is useful for selecting target polynucleotides, particularly polynucleotides which alter cell phenotypes of induce or inhibit cell death. The method can be used to isolate toxic genes such as tumour suppressors. The present sequence was used to illustrate the method of the the present invention.

Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;

Query Match 90.7%; Score 136; DB 22; Length 148;  
Best Local Similarity 98.7%; Pred. No. 8,4e-38;  
Matches 148; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 GGCCAAAATTTGAAAACTAGATCTATTATTGACGCGCGCCCATGACGTGATCCCC 60  
|  
Db 1 GGCCAAAATTTGAAAACTAGATCTATTATTGACGCGCGCCCATG--GTGGATCCCC 58  
QY 61 CGGGCTCAGGAATTCGATATCAAGCTTATCGATACCTCGAGGGGGGCTTAA 120  
|  
Db 59 CGGGCTCAGGAATTCGATATCAAGCTTATCGATACCTCGAGGGGGGCTTAA 118

```

OY      121 CTACTAATTTCTTTGTGGCGCGGCC 150
      |||||||
Db      119 CTACTAATTTGTGTTGTGGCGCGGCC 148

RESULT 9
AAD31779
ID      AAD31779 standard; DNA: 148 BP.
XX
AC      AAD31779;
XX
DT      18-JUN-2002 (first entry)
XX
DE      Modified p7.5/tk vector, p7.5/ATG1/tk.
XX
KW      Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;
KW      vaccine; immune response; cytosolic; p7.5/tk vector; thymidine kinase;
XX      p7.5/ATG1/tk vector; ds.
XX
OS      Vaccinia virus.
OS      Synthetic.
XX
FH      Key
FH      misc_signal
FT      46..48
FT      /tag= a
FT      /note= "translation start codon"
FT      116..118
FT      /tag= b
FT      /note= "translation stop codon"
FT      120..122
FT      /tag= c
FT      /note= "translation stop codon"
FT      124..126
FT      /tag= d
FT      /note= "translation stop codon"
FT      132..138
FT      /tag= e
FT      /note= "transcription stop signal"
FT
XX      US2002018785-A1.
XX      14-FEB-2002.
XX
PD      02-APR-2001: 2001US-0822250.
XX
XX      22-SEP-1997: 97US-0935377.
XX
PA      (UYRP ) UNIV ROCHESTER.
XX
PI      Zauderer M;
XX
DR      WPI: 2002-239252/29.
XX
PT      Representational Difference Analysis method for identification of
PT      antigens recognized by cytotoxic T cells and specific for human tumors,
PT      comprises improved selection of genes encoding target antigens
XX
PS      Example 1: Fig 2; 54pp: English.
XX
XX      The present invention relates to novel methods for the identification
XX      of antigens recognised by cytotoxic T cells (CTLs) and specific for
XX      human tumours, cancers and infected cells. The method involves screening
XX      the products of an expression library generated from DNA/RNA of a cell
XX      expressing a target epitope with cytotoxic T cells generated against
XX      the cell to identify DNA clones expressing target epitope or providing
XX      cytotoxic T cells specific for a gene product differentially expressed
XX      by a cell and measuring the cross-reactivity of the cytotoxic T cells
XX      for cells expressing a target epitope in which the target epitope is
XX      identified as a gene product inducing cytotoxic T cells. The method is
XX      useful for identifying a target epitope or antigen specific for a tumour
XX      cell. The target epitope is also useful for identifying target antigens
XX      in other target cells against which it is desirable to induce cell-

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CC      mediated immunity. The antigen identified by the method is useful
CC      in immunogenic compositions and vaccine preparations to induce the
CC      regression of tumours, cancers and infections in mammals. The invention
CC      also relates to vaccinia viral vectors which are useful for treating
CC      tumour-bearing mammals, including humans to generate immune response
CC      against the tumour cells. They are also useful for immunising or
CC      vaccinating tumour-free subjects to prevent tumour formation. The
CC      present sequence is modified p7.5/tk (thymidine kinase) vector,
CC      p7.5/ATG1/tk. This vector comprises a vaccinia virus 7.5k promoter and
CC      a modified tk DNA fragment. This vector is used in the exemplification
CC      of the invention.
XX
SO      Sequence 148 BP; 35 A; 37 C; 39 G; 37 T; 0 other;
XX
XX      Query Match          90.7%; Score 136; DB 24; Length 148;
XX      Best Local Similarity 98.7%; Pred No. 8.4e-38;
XX      Matches 148; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
OY      1 GGCAGAAATTTGAAATAGATCTATTATTGACGCGCGCGCATGACGTGATCCCC 60
      |||||||
Db      1 GGCAGAAATTTGAAATAGATCTATTATTGACGCGCGCGCATG--GTGGATCCCC 58
OY      61 CGGCTGCAGGATTCGATTCAGCTTATCGATACCGTGCAGGCGGCGCTTAA 120
      |||||||
Db      59 CGGCTGCAGGAAATTCGATTCAGCTTATCGATACCGTGCAGCTCGAGGGGCGCTTAA 118
OY      121 CTACTAATTTGTGTTGTGGCGCGGCC 150
      |||||||
Db      119 CTACTAATTTGTGTTGTGGCGCGGCC 148

RESULT 10
AAA15235
ID      AAA15235 standard; DNA: 145 BP.
XX
AC      AAA15235;
XX
DT      04-SEP-2000 (first entry)
XX
DE      Nucleotide sequence of a fragment of the plasmid p7.5/ATG0/tk.
XX
KW      Vaccinia transfer plasmid; epitope; tumour specific epitope; antigen;
KW      vaccine; tumour regression; cancer; infection; ss.
XX
OS      Synthetic.
XX
PD      WO200028016-A1.
XX
XX      18-MAY-2000.
XX
XX      10-NOV-1998; 98WO-US24029.
XX
XX      10-NOV-1998; 98WO-US24029.
XX
PA      (UYRP ) UNIV ROCHESTER.
XX
PI      Zauderer M;
XX
DR      WPI: 2000-376533/32.
XX
PT      Novel method of identifying target epitopes or antigens specific for
PT      human tumors, cancers and infected cells involving screening expression
PT      library products of a cell expressing the target epitope
XX
PS      Disclosure; Fig 2; 132pp: English.
XX
XX      The present sequence represents a fragment of a vaccinia transfer
XX      plasmid, which is used in the course of the invention. The
XX      specification describes a method for identifying a target epitope.
XX      The method comprises screening the products of an expression library
XX      from a cell expressing the target epitope with cytotoxic T cells
XX      generated against the cell to identify DNA clones expressing the target
XX      epitope. The method may also comprise providing a cytotoxic T cell

```



CC specific for a gene product differentially expressed by a cell and  
CC measuring the cross-reactivity of the cytotoxic T cell. The methods are  
CC useful for identifying tumour specific target epitopes and antigens which  
CC are useful in immunogenic compositions or vaccines to induce the  
CC regression of tumors, cancers or infections in mammals. The genes  
CC expressed in a panel of tumour cells that are derived from single  
CC immortalised, non-tumorigenic cell line are used to generate HLA  
CC restricted cytotoxic T cells which are evaluated for activity against  
CC tumour cells. The method is useful to identify potential antigens  
CC expressed not only by the pathogen but also by the host cells whose gene  
CC expression is altered as a result of infection. The differential gene  
CC expression strategies can be applied to identify immunogenic molecules  
CC of cells infected with virus, fungus or mycobacterium.

SO Sequence 145 BP; 34 A; 37 C; 38 G; 36 T; 0 other;

Query Match 86.7%; Score 130; DB 21; Length 145;  
Best Local Similarity 96.7%; Pred. No. 1,1e-35;  
Matches 145; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 GGGCAAAATTTGAAAACTGATCTATTATTGTCACGCGCGCCCATGACGTGATCCCC 60  
DB 1 GGGCAAAATTTGAAAACTGATCTATTATTGTCACGCGCGCCCATGACGTGATCCCC 55  
QY 61 CGGGCTCAGAGATTCGATTCAGCTTATTCGATACCGTCGACCTCGAGGGGGGCTTAA 120  
DB 56 CGGGCTCAGAGATTCGATTCAGCTTATTCGATACCGTCGACCTCGAGGGGGGCTTAA 115  
QY 121 CTAACCTAATTTTGTGTTGTGGCGCGGCC 150  
DB 116 CTAACCTAATTTTGTGTTGTGGCGCGGCC 145

## RESULT 11

ABA01476  
ID ABA01476 standard; DNA; 145 BP.

AC ABA01476;

DT 04-FEB-2002 (first entry)

DE Partial p7.5/ATG0/tk sequence.

KW Cell death; toxic gene; tumour suppressor; ds.

OS Synthetic.

PN W0200172995-A2.

PD 04-OCT-2001.

PF 28-MAR-2001; 2001WO-US09953.

PR 28-MAR-2000; 2000US-0192586.

PR 10-MAY-2000; 2000US-0203343.

PR 23-JAN-2001; 2001US-0263226.

PR 27-FEB-2001; 2001US-0271426.

PA (UVRP ) UNITV ROCHESTER.

PI Zauderer M, Smith ES;

DR WPI; 2001-570897/64.

PT Selecting target polynucleotides, particularly toxic genes, involves

PT introducing a library of insert polynucleotides into a host cell

PT population, where the target polynucleotide promotes cell death -

PS Disclosure: Fig 8; 359pp; English.

XX The present invention relates to a method for selecting a target

CC polynucleotide. The method comprises introducing into a host cell

CC population a library of insert polynucleotides, where expression of the

CC target polynucleotide directly or indirectly promotes host cell death.  
CC The cells are cultured and the insert polynucleotides are collected from  
CC the cells which die. The method is useful for selecting target  
CC polynucleotides, particularly polynucleotides which alter cell phenotypes  
CC of induce or inhibit cell death. The method can be used to isolate toxic  
CC genes such as tumour suppressors. The present sequence was used to  
CC illustrate the method of the the present invention.

SO Sequence 145 BP; 34 A; 37 C; 38 G; 36 T; 0 other;

Query Match 86.7%; Score 130; DB 22; Length 145;  
Best Local Similarity 96.7%; Pred. No. 1,1e-35;  
Matches 145; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 GGGCAAAATTTGAAAACTGATCTATTATTGTCACGCGCGCCCATGACGTGATCCCC 60  
DB 1 GGGCAAAATTTGAAAACTGATCTATTATTGTCACGCGCGCCCATGACGTGATCCCC 55  
QY 61 CGGGCTCAGAGATTCGATTCAGCTTATTCGATACCGTCGACCTCGAGGGGGGCTTAA 120  
DB 56 CGGGCTCAGAGATTCGATTCAGCTTATTCGATACCGTCGACCTCGAGGGGGGCTTAA 115  
QY 121 CTAACCTAATTTTGTGTTGTGGCGCGGCC 150  
DB 116 CTAACCTAATTTTGTGTTGTGGCGCGGCC 145

## RESULT 12

AAD31778  
ID AAD31778 standard; DNA; 145 BP.

AC AAD31778;

DT 18-JUN-2002 (first entry)

DE Modified p7.5/tk vector, p7.5/ATG0/tk.

KW Cytotoxic T cell; CTL; tumour; cancer; infection; cell-mediated immunity;

KW vaccine; immune response; cytostatic; p7.5/tk vector; thymidine kinase;

KW p7.5/ATG0/tk vector; ds.

OS Vaccinia virus.

OS Synthetic.

EH Key

FT misc\_signal Location/Qualifiers

FT 113..115 /tag= a

FT /note= "Translation stop codon"

FT 117..119 /tag= b

FT /note= "Translation stop codon"

FT 121..123 /tag= c

FT /note= "Translation stop codon"

FT 129..135 /tag= d

FT /note= "Transcription stop signal"

US2002018785-A1.

14-FEB-2002.

02-APR-2001; 2001US-0822250.

22-SEP-1997; 97US-0935377.

(UVRP ) UNITV ROCHESTER.

Zauderer M;

WPI; 2002-239252/29.

Representational Difference Analysis method for identification of



PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAY-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
PI Schlegel R, Endege WO, Monahan JE;  
XX WPI; 2001-662795/76.  
XX  
XX Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer -  
XX  
PS Claim 1: Page 7801; 11750pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
SQ Sequence 432 BP; 118 A; 103 C; 105 G; 106 T; 0 other:  
Query Match 49.9%; Score 74.8; DB 23; Length 432;  
Best Local Similarity 72.4%; Pred. No. 3.2e-16;  
Matches 97; Conservative 0; Mismatches 37; Indels 0; Gaps 0;  
QY 2 GCCAATAATTTGAATAAGATCTATTATGACGCGCGCCGCGCATGACGTGATCCGCC 61  
DB 172 GCAAAATAGTTAAATTAACAAATTTGACCTCGCGCTCTAGAACTAGTGATCCGCC 231  
QY 62 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGCAGCTCGAGGGGGGCGCTAAC 121  
DB 233 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGCAGCTCGAGGGGGGCGCGGT 291  
QY 122 TAACTAATTTGTT 135  
DB 292 ACCCAGCTTTGTT 305  
RESULT 15  
ABV39281  
ID ABV39281 standard; CDNA; 508 BP.  
XX  
XX ABV39281;  
AC  
XX 16-SEP-2002 (first entry)  
DT  
XX  
XX Human prostate expression marker cDNA 39272.  
DE  
XX  
XX Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;  
KW pharmacogenomic marker; gene; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200160860-A2.  
PN  
XX 23-AUG-2001.  
PD  
XX  
PF 20-FEB-2001; 2001WO-US05171.

XX  
PR 17-FEB-2000; 2000US-183319P.  
PR 16-MAR-2000; 2000US-189862P.  
PR 25-MAY-2000; 2000US-207454P.  
PR 09-JUN-2000; 2000US-211314P.  
PR 18-JUL-2000; 2000US-219007P.  
PR 13-DEC-2000; 2000US-255281P.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
PI Schlegel R, Endege WO, Monahan JE;  
XX WPI; 2001-662795/76.  
XX  
XX Novel isolated nucleic acid molecule associated with cancerous state of  
PT prostate cells and correlating with presence of prostate cancer, useful  
PT for detecting presence of prostate cancer, stage of prostate cancer -  
XX  
PS Claim 1: Page 7972; 11750pp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule (I) comprising  
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the  
CC specification or its complement. (I) is useful for:  
CC (a) assessing whether a patient is afflicted with prostate cancer;  
CC (b) monitoring the progression of prostate cancer in a patient;  
CC (c) assessing the efficacy of a test compound to inhibit prostate  
CC cancer in a patient;  
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer  
CC in a patient;  
CC (e) selecting a composition for inhibiting prostate cancer in a patient;  
CC (f) assessing the prostate cell carcinogenic potential of a compound;  
CC (g) determining whether prostate cancer has metastasized in a patient;  
CC (h) assessing the aggressiveness or indolence of prostate cancer in a  
CC patient;  
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.  
SQ Sequence 508 BP; 140 A; 115 C; 125 G; 128 T; 0 other:  
Query Match 49.6%; Score 74.4; DB 23; Length 508;  
Best Local Similarity 72.7%; Pred. No. 4.7e-16;  
Matches 96; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
QY 4 CAAAATTTGAATAACTATCTATTATTGACGCGCGCGCCGCGCATGACGTGATCCCGCG 63  
DB 173 CAAAAGGACAGTTTAAATTTGTACCTGCGCGCGCGCTCGAAGTGCATCCCGCG 232  
QY 64 GCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGCAGCTCGAGGGGGGCGCTAACTA 123  
DB 233 GCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGCAGCTCGAGGGGGGCGCGTAC 292  
QY 124 ACTAATTTGTT 135  
DB 293 CCAGCTTTGTT 304

Search completed: November 10, 2002, 05:58:29  
Job time: 177.987 secs



RESULT 2  
US-09-987-456-5  
; Sequence 5, Application US/09987456  
; Patent No. US20020123057A1  
; GENERAL INFORMATION:

```
APPLICANT: University of Rochester
APPLICANT: Zauderer, Maurice
APPLICANT: Ernest S. Smith
TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
FILE REFERENCE: 1821.0070004
CURRENT APPLICATION NUMBER: US/09/987,456
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/271,424
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 60/262,067
PRIOR FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/298,087
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/249,268
PRIOR FILING DATE: 2000-11-17
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 150
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: p7.5/ATG3/lk vector
US-09-987-456-5

Query Match
Best Local Similarity 100.0%; Score 150; DB 10; Length 150;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GGGCAAAAATGAAAACAGATCTATTATTGACGCGCGCGCCGACGATGATCCCC 60
DB 1 GGGCAAAAATGAAAACAGATCTATTATTGACGCGCGCGCCGACGATGATCCCC 60
QY 61 CGGGCTGCAGGAATTCGATATCAAGCTTATCGATCCGTCGACCTCGAGGGGGGCGCTAA 120
DB 61 CGGGCTGCAGGAATTCGATATCAAGCTTATCGATCCGTCGACCTCGAGGGGGGCGCTAA 120
QY 121 CTAACATAATTTGTTTGTGGGCCCGGCC 150
DB 121 CTAACATAATTTGTTTGTGGGCCCGGCC 150

RESULT 3
US-09-822-250-8
; Sequence 8, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 149
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-822-250-8
```

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Query Match 92.0%; Score 138; DB 10; Length 149;
Best Local Similarity 99.3%; Pred. No. 7e-43;
Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

QY 1 GGGCAAAAATGAAAACAGATCTATTATTGACGCGCGCGCCGACGATGATGATCCCC 60  
DB 1 GGGCAAAAATGAAAACAGATCTATTATTGACGCGCGCGCCGACATGA-GTGGATCCCC 59  
QY 61 CGGGCTGCAGGAATTCGATATCAAGCTTATCGATCCGTCGAGGGGGGCGCTAA 120  
DB 121 CTAACATAATTTGTTTGTGGGCCCGGCC 150

```
DB 60 CGGGCTGCAGGAATTCGATATCAAGCTTATCGATCCGTCGACCTCGAGGGGGGCGCTAA 119
QY 121 CTAACATAATTTGTTTGTGGGCCCGGCC 150
DB 120 CTAACATAATTTGTTTGTGGGCCCGGCC 149

RESULT 4
US-09-987-456-4
; Sequence 4, Application US/09987456
; Patent No. US20020123057A1
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; APPLICANT: Ernest S. Smith
; TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
; TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
; FILE REFERENCE: 1821.0070004
; CURRENT APPLICATION NUMBER: US/09/987,456
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/271,424
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/262,067
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/298,087
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/249,268
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 149
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p7.5/ATG2/lk vector
US-09-987-456-4
```

```
Query Match 92.0%; Score 138; DB 10; Length 149;
Best Local Similarity 99.3%; Pred. No. 7e-43;
Matches 149; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
```

QY 1 GGGCAAAAATGAAAACAGATCTATTATTGACGCGCGCGCCGACGATGATCCCC 60  
DB 1 GGGCAAAAATGAAAACAGATCTATTATTGACGCGCGCGCCGACATGA-GTGGATCCCC 59  
QY 61 CGGGCTGCAGGAATTCGATATCAAGCTTATCGATCCGTCGACCTCGAGGGGGGCGCTAA 120  
DB 61 CGGGCTGCAGGAATTCGATATCAAGCTTATCGATCCGTCGACCTCGAGGGGGGCGCTAA 119  
QY 121 CTAACATAATTTGTTTGTGGGCCCGGCC 150  
DB 120 CTAACATAATTTGTTTGTGGGCCCGGCC 149

```
RESULT 5
US-09-822-250-7
; Sequence 7, Application US/09822250
; Patent No. US20020018785A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
; TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
; FILE REFERENCE: 1821.0010001
; CURRENT APPLICATION NUMBER: US/09/822,250
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 08/935,377
; PRIOR FILING DATE: 1997-09-22
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 148
; TYPE: DNA
; ORGANISM: synthetic construct
```

US-09-822-254-7

Query Match	90.7%;	Score 136;	DB 10;	Length 148;
Best Local Similarity	98.7%;	Pred. No. 4e-42;		
Matches 148;	Conservative	0;	Mismatches	0;
			Indels	2;
			Gaps	1

[illegible]

RESULT 6  
US-09-987-456-3

```

? GENERAL INFORMATION:
? APPLICANT: University of Rochester
? APPLICANT: Zauderer, Maurice
? APPLICANT: Ernest S. Smith
? TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
? TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
? FILE REFERENCE: 1821.0070004
? CURRENT APPLICATION NUMBER: US/09/987,456
? PRIOR FILING DATE: 2001-11-14
? PRIOR APPLICATION NUMBER: 60/271,424
? PRIOR FILING DATE: 2001-02-27
? PRIOR APPLICATION NUMBER: 60/262,067
? PRIOR FILING DATE: 2001-01-18
? PRIOR APPLICATION NUMBER: 60/298,087
? PRIOR FILING DATE: 2001-06-15
? PRIOR APPLICATION NUMBER: 60/249,268
? PRIOR FILING DATE: 2000-11-17
? NUMBER OF SEQ ID NOS: 147
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 3
? LENGTH: 148
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: p 7.5/ATGI/tk promoter
? -S-09-987-456-3

```

Query Match	90.7%;	Score 136;	DB 10;	Length 148;
Best Local Similarity	98.7%;	Pred. No. 4e-42;		
Matches 148; Conservative	0;	Mismatches	0;	Indels 2; Gaps 1;

QY	1	6GCCAAAATTTGAAAACATCATCATTTATTTATTCGACGGGGCCGACATGACGTGCATCC	60
Db	1	GGCCAAAATTTGAAAACATCATCATTTATTTATTCGACGGGGCCGACATGACGTGCATCC	58
QY	61	CGGGCTGAGAGAAATTCATATCAACGCTTATGATACCGTCGACCTCGAGGGGGGGCCTAA	120
Db	59	CGGGCTGAGAGAAATTCATATCAACGCTTATGATACCGTCGACCTCGAGGGGGGGCCTAA	118
QY	121	CTAACTAAATTTGTTTTGTGTGGGCCCGGCC	150
Db	119	CTAACTAAATTTGTTTTGTGTGGGCCCGGCC	148

RESULT 7  
US-09-822-250-6  
; Sequence 6, Application US/09822250  
; Patent No. US20020018785A1  
; GENERAL INFORMATION:  
; APPLICANT: Zauderer, Maurice

```

? TITLE OF INVENTION: Methods for Producing Recombinant Libraries in Vaccinia Virus
? FILE REFERENCE: 1821.0010001
? CURRENT APPLICATION NUMBER: US/09/822,250
? CURRENT FILING DATE: 2001-04-02
? PRIOR APPLICATION NUMBER: US 08/935,377
? PRIOR FILING DATE: 1997-09-22
? NUMBER OF SEQ ID NOS: 37
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 6
? LENGTH: 145
? TYPE: DNA
? ORGANISM: synthetic construct
US-09-822-250-6

Query Match      86.7%   Score 130;   DB 10;   Length 145;
Best Local Similarity 96.7%   Pred. No. 7,4e-40;
Matches 145; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

```

Query Match	86.7%;	Score 130;	DB 10;	Length 145;
Best Local Similarity	96.7%;	Pred. No. 7.4e-40;		
Matches 145;	Conservative	0;	Mismatches 0;	Indels 5; Gaps 1;

Oy	1	GGCCCCAAATTTGAAAACCAATTAATCATATTTATTTATTTGGACGGGGCCGACATAGACGTGGATATCC	60
Db	1	GGCCAAAATTTGAAAACCAATTAATCATATTTATTTATTTGGACGGGGCCGACG-----CGTGGATCCCC	55
Oy	61	CGGGGTGAGAAATTCATATCAACGCTTATGTGATACCGCTGGACCTCGACGGGGGGGCGCTAA	120
Db	56	CGGGGTGAGAAATTCATATCAACGCTTATGTGATACCGCTGGACCTCGAGGGGGGGCGCTAA	115
Oy	121	CTAACTAAATTTGTTTTGTGTGGGGCCGGCC	150
Db	116	CTAACTAAATTTGTTTTGTGTGGGGCCGGCC	145

```

; RESULT 8
; US-09-987-456-2
; Sequence 2, Application US/09987456
; Patent No. US20020123057A1
; GENERAL INFORMATION:
; APPLICANT: University of Rochester
; APPLICANT: Zauderer, Maurice
; APPLICANT: Ernest S. Smith
; TITLE OF INVENTION: In Vitro Methods Of Producing And Selecting
; TITLE OF INVENTION: Immunoglobulin Molecules In Eukaryotic Cells
; FILE REFERENCE: 1821.0070004
; CURRENT APPLICATION NUMBER: US/09/987,456
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/271,424
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/262,067
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/298,087
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/249,268
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 145
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p 7.5/ATG0/tk promoter
; US-09-987-456-2

```

Query Match	86.7%;	Score 130;	DB 10;	Length 145;
Best Local Similarity	96.7%;	Pred. No. 7.4e-40;		
Matches 145; Conservative	0;	Mismatches 0;	Indels 5;	Gaps 1;

QY	1	GGGCAAAATTTGAAAACCTAGATCTATTTTTCACGGGGCCCATGACGTGATCTCCC	60
Db	1	GGGCAAAATTTGAAAACCTAGATCTATTTTTCACGGGGCCCATGACGTGATCTCCC	55
QY	61	CGGGCTGCAGGATTCGATTCATCAAGCTTATCGATTACCGTCGACCTCGAGGGGGGGCTTAA	120
Db	56	CGGGCTGCAGGATTCGATTCATCAAGCTTATCGATTACCGTCGACCTCGAGGGGGGGCTTAA	115





US-09-850-746A-306

Query Match  
Best Local Similarity 44.7%; Score 67; DB 10; Length 457;  
100.0%; Pred. No. 8.4e-16;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 GTGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACTCGAGG 110  
|||||  
DB 360 GTGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACTCGAGG 419  
OY 111 GGGGGCC 117  
|||||  
DB 420 GGGGGCC 426

RESULT 13

US-09-897-778-306  
Sequence 306, Application US/09897778  
Patent No. US20020147143A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Marnierakis, Margarita  
APPLICANT: Fanger, Gary R.  
APPLICANT: Veevick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Watanabe, Yoshihiro  
APPLICANT: Henderson, Robert A.  
APPLICANT: Peckham, David W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C16  
CURRENT APPLICATION NUMBER: US/09/897,778  
CURRENT FILING DATE: 2001-06-28  
NUMBER OF SEQ ID NOS: 467  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 306  
LENGTH: 457  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-897-778-306

Query Match  
Best Local Similarity 44.7%; Score 67; DB 10; Length 457;  
100.0%; Pred. No. 8.4e-16;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 GTGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACTCGAGG 110  
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DB 360 GTGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACTCGAGG 419  
OY 111 GGGGGCC 117  
|||||  
DB 420 GGGGGCC 426

RESULT 14

US-09-956-004-108/C  
Sequence 108, Application US/09956004  
Patent No. US2002072595A1  
GENERAL INFORMATION:  
APPLICANT: Patrick J. Dillon et al.  
TITLE OF INVENTION: Nucleotide Sequences of Escherichia coli Pathogenicity Islands  
FILE REFERENCE: PB324D1  
CURRENT APPLICATION NUMBER: US/09/956,004  
CURRENT FILING DATE: 2001-09-20  
PRIOR APPLICATION NUMBER: 08/976,259  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/061,953  
PRIOR FILING DATE: 1997-10-14  
PRIOR APPLICATION NUMBER: 60/031,626  
PRIOR FILING DATE: 1996-11-22  
NUMBER OF SEQ ID NOS: 142  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 108  
LENGTH: 752  
TYPE: DNA  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (714)..(714)  
OTHER INFORMATION: n equals a, t, g, or c  
NAME/KEY: misc\_feature  
LOCATION: (719)..(719)  
OTHER INFORMATION: n equals a, t, g, or c  
US-09-956-004-108

Query Match  
Best Local Similarity 44.7%; Score 67; DB 10; Length 752;  
100.0%; Pred. No. 1.1e-15;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 GTGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACTCGAGG 110  
|||||  
DB 72 GTGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACTCGAGG 13  
OY 111 GGGGGCC 117  
|||||  
DB 12 GGGGGCC 6

RESULT 15

US-09-735-705-91  
Sequence 91, Application US/09735705  
Patent No. US20020052329A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.455C14  
CURRENT APPLICATION NUMBER: US/09/735,705  
CURRENT FILING DATE: 2000-12-12  
NUMBER OF SEQ ID NOS: 419  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 91  
LENGTH: 858  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(858)  
OTHER INFORMATION: n = A,T,C or G  
US-09-735-705-91

Query Match  
Best Local Similarity 44.7%; Score 67; DB 10; Length 858;  
100.0%; Pred. No. 1.1e-15;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 GTGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACTCGAGG 110  
|||||  
DB 357 GTGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACTCGAGG 416  
OY 111 GGGGGCC 117  
|||||  
DB 417 GGGGGCC 423

Tue Nov 12 06:25:51 2002

us-08-935-377-9.rnpb

Page 6

Search completed: November 10, 2002, 11:33:47  
Job time : 38.3313 secs

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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 05:43:30 ; Search time 38.4558 Seconds

(without alignments)  
1196.219 Million cell updates/sec

Title: US-08-935-377-9

Perfect score: 150

Sequence: 1 GGGCCAAATATGAAAAACTA.....TTGTTTGTGGCCGGCCG 150

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued\_Patents\_NA.\*  
2: /cgn2\_6/ptodata/1/1na/5A.COMB.seq.\*  
3: /cgn2\_6/ptodata/1/1na/5B.COMB.seq.\*  
4: /cgn2\_6/ptodata/1/1na/6A.COMB.seq.\*  
5: /cgn2\_6/ptodata/1/1na/6B.COMB.seq.\*  
6: /cgn2\_6/ptodata/1/1na/6C.COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69.8	46.5	793	2	US-08-967-101-121 Sequence 121, App
2	69.8	46.5	793	2	US-08-992-941-121 Sequence 121, App
3	69.8	46.5	793	3	US-09-124-698-121 Sequence 121, App
4	69.8	46.5	793	4	US-09-127-480-121 Sequence 121, App
5	69.8	46.5	793	4	US-08-496-841C-121 Sequence 121, App
6	69.8	46.5	793	4	US-09-124-523-121 Sequence 121, App
7	69.8	46.0	229	4	US-09-116-492A-39 Sequence 39, App1
8	67	44.7	147	4	US-09-323-872A-26 Sequence 306, App
9	67	44.7	457	4	US-09-643-597-306 Sequence 108, App
10	67	44.7	752	4	US-08-976-259-108 Sequence 91, App1
11	67	44.7	858	4	US-09-123-912-91 Sequence 91, App1
12	67	44.7	2961	4	US-08-946-935-6 Sequence 6, App1
13	67	44.7	3792	2	US-08-992-334-1 Sequence 1, App1
14	67	44.7	3792	2	US-08-992-334-1 Sequence 1, App1
15	67	44.7	3792	2	US-08-992-334-1 Sequence 1, App1
16	67	44.7	4016	1	US-08-410-540-3 Sequence 3, App1
17	67	44.7	5234	2	US-08-992-334-2 Sequence 2, App1
18	67	44.7	5234	2	US-08-992-334-2 Sequence 2, App1
19	67	44.7	5592	4	US-09-495-797-37 Sequence 37, App1
20	67	44.7	6722	2	US-08-992-334-3 Sequence 3, App1
21	67	44.7	6722	3	US-08-992-334-3 Sequence 3, App1
22	66.8	44.5	545	4	US-08-991-789A-10 Sequence 10, App1
23	66.8	44.5	545	4	US-09-062-451-10 Sequence 10, App1
24	66.8	44.5	545	4	US-09-598-326-10 Sequence 10, App1
25	66.2	44.1	9318	2	US-08-793-610-6 Sequence 6, App1
26	66.2	44.1	11233	4	US-08-980-832-27 Sequence 27, App1
27	65.8	43.9	6596	4	US-09-575-602-11 Sequence 11, App1

C	28	65.4	43.6	5356	4	US-08-446-935-1	Sequence 1, App1
C	29	65	43.3	78	4	US-09-462-645C-25	Sequence 25, App1
C	30	65	43.3	84	4	US-09-462-645C-26	Sequence 26, App1
C	31	65	43.3	698	4	US-08-998-416-54	Sequence 54, App1
C	32	65	43.3	3465	4	US-09-462-645C-9	Sequence 9, App1
C	33	65	43.3	3481	4	US-09-462-645C-11	Sequence 11, App1
C	34	65	43.3	3794	4	US-09-462-645C-5	Sequence 5, App1
C	35	65	43.3	3810	4	US-09-462-645C-7	Sequence 7, App1
C	36	64.4	42.9	713	4	US-08-998-416-135	Sequence 135, App1
C	37	62.4	41.6	685	1	US-08-463-115-56	Sequence 56, App1
C	38	62.4	41.6	685	1	US-08-465-388-56	Sequence 56, App1
C	39	59	39.3	4164	2	US-08-204-675-1	Sequence 1, App1
C	40	59	39.3	4164	2	US-08-660-754-1	Sequence 1, App1
C	41	59	39.3	4164	2	US-08-796-364-1	Sequence 1, App1
C	42	59	39.3	4164	2	PCT-US95-02520-1	Sequence 1, App1
C	43	58	38.7	5178	2	US-08-474-169-2	Sequence 2, App1
C	44	57.8	38.5	3198	4	US-08-842-306B-48	Sequence 48, App1
C	45	57.8	38.5	3198	4	US-08-838-973B-48	Sequence 48, App1

## ALIGNMENTS

```
RESULT 1
US-08-967-101-121/c
; Sequence 121, Application US/08967101
; Patent No. 5840540
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLUP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBAUT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,101
; FILING DATE: 10-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 793 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-967-101-121

Query Match      46.5%  Score 69.8; DB 2; Length 793;
Best Local Similarity 82.5%; Pred. No. 1.2e-15;
Matches 80; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
39 GGGCGGCGATGAGTGGATCCCGGGGCGGCGAGATGATGATCAAGCTTATCCATCCG 98
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Db 130 GGAGGCGCGGGGCGGATCCCCGGGCTGCGAGATTGGATATCAGCTTATCGATACCG 7  
Oy 99 TCGACCTCGAGGGGGGCGCTAATACTAATTGTGTT 135  
70 TCGACCTCGAGGGGGGCGGCTAATCCAGCTTTGTT 34

RESULT 2  
US-08-592-541-121/c  
; Sequence 121, Application US/08592541  
; Patent No. 5986054  
GENERAL INFORMATION:

```

1 GENERAL INFORMATION:
2 APPLICANT: ST. GEORGE-HYSLÖP, PETER H
3 APPLICANT: ROMMENS, JOHANNA M
4 APPLICANT: PRASER, PAUL E
5 TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
6 TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
7 NUMBER OF SEQUENCES: 183
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: TESPA, HUMWITZ & THIBEAULT
10 STREET: High Street Tower - 125 High Street
11 CITY: Boston
12 STATE: Massachusetts
13 COUNTRY: U.S.A.
14 ZIP: 02110
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: PatentIn Release #1.0, Version #1.30
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/592,541
22 FILING DATE:
23 CLASSIFICATION: 800
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Pletcher, Edmund R.
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (617) 248-7000
28 TELEFAX: (617) 248-7100
29 INFORMATION FOR SEQ. ID NO.: 121:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 793 base pairs
32 TYPE: nucleic acid
33 STRANDEDNESS: single
34 TOPOLOGY: linear
35 MOLECULE TYPE: DNA (genomic)
36
37 US-08-592-541-121

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Query Match	46.5%;	Score 69.8;	DB 2;	Length 793;
Best Local Similarity	82.5%;	Pred. No. 1.2e-15;		
Matches 80;	Conservative	0;	Mismatches 17;	Indels 0;
				Gaps 0

OY	39	GGGCCGCATGACGTGGATTCCCCCGGGCTGACAGAAATTGATCAACTAATGATACCG	98
Dd	130	GGAGGCCGGCGGGGGGATCCCCCGGGCTGACAGAAATTGATATCAAGTTATGATACCG	71
OY	99	TGCAGCTCGAGGGGGGGCCTTAACATACTAATTTTGT	135
Dd	70	TCGACCTCGAGGGGGGGGCCGGATACCAGCTTTTITT	34

RESULT 3  
US-09-124-698-121/c  
; Sequence 121, Application US/09124698  
; Patent No. 6117978

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ADDRESS: TESTA, HURWITZ & THIEBAULT  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/124,698  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/592,541  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pitcher, Edmund R.  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 248-7000  
TELEFAX: (617) 248-7100  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 793 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-124-698-121

Query Match	46.5%;	Score 69.8;	DB 3;	Length 793;
Best Local Similarity	82.5%;	Pred. No. 1.2e-15;		
Matches	80;	Conservative	0;	Mismatches 17;
			Indels	0;
			Gaps	0;

[illegible]

RESULT 4  
US-09-127-480-121/c  
; Sequence 121, Application US/09127480

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Query Match 46.58; Score 69.8; DB 4; Length 793.

Sequence 39, Application US/09116492A

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; GENERAL INFORMATION:
; APPLICANT: GICOUEL, BRIGITTE
; APPLICANT: BERTHET, FRANCOIS-XAVIER
; APPLICANT: ANDERSEN, PETER
; APPLICANT: RASMUSSEN, PETER B
; TITLE OF INVENTION: POLYNUCLEOTIDE FUNCTIONALLY CODING FOR THE LHP PROTEIN FROM MYCOE
; TITLE OF INVENTION: TUBERCULOSIS, ITS BIOLOGICALLY ACTIVE DERIVATIVE FRAGMENTS, AS W
; TITLE OF INVENTION: USING THE SAME
; FILE REFERENCE: 0660-0137-27X
; CURRENT APPLICATION NUMBER: US/09/116,492A
; CURRENT FILING DATE: 1998-07-16
; PRIOR APPLICATION NUMBER: 60/252,631
; PRIOR FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: multiple cloning site-artificial DNA
US-09-116-492A-39

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Query Match
Best Local Similarity 46.0%; Score 69; DB 4; Length 229;
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 51 GTGATCCCCCGGCTGCAGAAATTCGATATCAAGCTTATGATACCGTCGACCTCGAGG 110
Db 140 GTGATCCCCCGGCTGCAGAAATTCGATATCAAGCTTATGATACCGTCGACCTCGAGG 81

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QY 111 GGGGGCCTACTACTAATTGTT 135
Db 80 GGGGGCCCGGTACCACTTTTGT 56

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RESULT 8
US-09-323-872A-26/C
; Sequence 26, Application US/09323872A
; Patent No. 6395539
; GENERAL INFORMATION:
; APPLICANT: Coschigano, Peter
; TITLE OF INVENTION: Compositions and Methods for Bioremediation
; FILE REFERENCE: OHU-03640
; CURRENT APPLICATION NUMBER: US/09/323,872A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/072,433
; PRIOR FILING DATE: 1998-05-04
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 147
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(147)
US-09-323-872A-26

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Query Match
Best Local Similarity 44.7%; Score 67; DB 4; Length 147;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 51 GTGATCCCCCGGCTGCAGAAATTCGATATCAAGCTTATGATACCGTCGACCTCGAGG 110
Db 106 GTGATCCCCCGGCTGCAGAAATTCGATATCAAGCTTATGATACCGTCGACCTCGAGG 47

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QY 111 GGGGGCC 117
Db 46 GGGGGCC 40

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RESULT 9

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US-09-643-597-306
; Sequence 306, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy R.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121,455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 306
; LENGTH: 457
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-643-597-306

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Query Match
Best Local Similarity 44.7%; Score 67; DB 4; Length 457;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 51 GTGATCCCCCGGCTGCAGAAATTCGATATCAAGCTTATGATACCGTCGACCTCGAGG 110
Db 360 GTGATCCCCCGGCTGCAGAAATTCGATATCAAGCTTATGATACCGTCGACCTCGAGG 419

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QY 111 GGGGGCC 117
Db 420 GGGGGCC 426

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RESULT 10
US-08-976-259-108/C
; Sequence 108, Application US/08976259
; Patent No. 6316609
; GENERAL INFORMATION:
; APPLICANT: Dillon, Patrick J.
; APPLICANT: Choi, Gil H.
; APPLICANT: Welch, Rodney A.
; TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
; Patent No. 6316609
; NUMBER OF SEQUENCES: 142
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,259
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
; ATTORNEY/AGENT INFORMATION:
; NAME: Steife, Eric K.
; REGISTRATION NUMBER: 36,688

```

```
REFERENCE/DOCKET NUMBER: 1488.0740002/EKS/CEM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-976-259-108

Query Match
Best Local Similarity 44.7%; Score 67; DB 4; Length 752;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GTGATCCCCGGGCTGCAGATTCGATTCAGCTTATGACCTGACCTGCAGG 110
Db 72 GTGATCCCCGGGCTGCAGATTCGATTCAGCTTATGACCTGACCTGCAGG 13
Qy 111 GGGGGCC 117
Db 12 GGGGGCC 6

RESULT 11
US-09-123-912-91
Sequence 91, Application US/09123912A
Patent No. 6312695
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REFERENCE: 210121.455C1
CURRENT APPLICATION NUMBER: US/09/123,912A
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: 09/040,802
NUMBER OF SEQ ID NOS: 114
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 91
LENGTH: 858
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (570)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (591)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (655)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (664)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (667)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (683)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (711)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (739)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (760)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
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LOCATION: (765)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (777)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (787)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (792)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (794)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (801)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (804)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (809)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (817)
OTHER INFORMATION: Where n is a, c, g or t
NAME/KEY: modified_base
LOCATION: (820)
OTHER INFORMATION: Where n is a, c, g or t
US-09-123-912-91

Query Match
Best Local Similarity 44.7%; Score 67; DB 4; Length 858;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 GTGATCCCCGGGCTGCAGATTCGATTCAGCTTATGACCTGACCTGCAGG 110
Db 357 GTGATCCCCGGGCTGCAGATTCGATTCAGCTTATGACCTGACCTGCAGG 416
Qy 111 GGGGGCC 117
Db 417 GGGGGCC 423

RESULT 12
US-09-643-597-91
Sequence 91, Application US/09643597
Patent No. 6426072
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 91
LENGTH: 858
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
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LOCATION: (1)...(858)  
OTHER INFORMATION: n = A,T,C or G  
US-09-643-597-91

Query Match 44.7%; Score 67; DB 4; Length 858;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 GTGATCCCGGGGCTGACGAATTCATATCCCTGACCTCGAGG 110  
DB 357 GTGATCCCGGGGCTGACGAATTCATATCCCTGACCTCGAGG 416  
OY 111 GGGGGCC 117  
DB 417 GGGGGCC 423

## RESULT 13

US-08-446-935-6/c  
Sequence 6, Application US/08446935

Patent No. 6187991

GENERAL INFORMATION:  
APPLICANT: Soeller, Walter C.

APPLICANT: Carty, Maynard D.

TITLE OF INVENTION: TRANSGENIC ANIMAL MODELS FOR TYPE II

TITLE OF INVENTION: DIABETES MELLITUS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pfizer Inc.

STREET: 235 East 42nd Street, 20th Floor

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10017-5755

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,935

FILING DATE:  
CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:  
NAME: Sheyka, Robert F.

REGISTRATION NUMBER: 31,304

REFERENCE/DOCKET NUMBER: PC8153

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)573-1189

TELEFAX: (212)573-1939

TELEX: N/A

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:  
LENGTH: 2961 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

US-08-446-935-6

Query Match 44.7%; Score 67; DB 4; Length 2961;  
Best Local Similarity 100.0%; Pred. No. 1.8e-14;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 GTGATCCCGGGGCTGACGAATTCATATCCCTGACCTCGAGG 110  
DB 726 GTGATCCCGGGGCTGACGAATTCATATCCCTGACCTCGAGG 667  
OY 111 GGGGGCC 117  
DB 666 GGGGGCC 660

## RESULT 14

US-08-992-334-1/c  
Sequence 1, Application US/08992334

Patent No. 5919678

GENERAL INFORMATION:  
APPLICANT: Gruss, Alexandra

APPLICANT: Maguin, Emmanuelle

TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Christie Parker & Hale, LLP

STREET: 350 West Colorado Boulevard, Suite 500

CITY: Pasadena

STATE: California

COUNTRY: United States

ZIP: 91105

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/992,334

FILING DATE: 17-DEC-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/302,752

FILING DATE: 24-DEC-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR93/00248

FILING DATE: 12-MAR-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 992/03034

FILING DATE: 13-MAR-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Prout, D. Bruce

REGISTRATION NUMBER: 20958

REFERENCE/DOCKET NUMBER: C93:31779

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (626) 795-9900

TELEFAX: (626) 577-8800

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 3792 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOHETICAL: NO

ANTI-SENSE: YES

IMMEDIATE SOURCE:  
CLONE: pg+host4

US-08-992-334-1

Query Match 44.7%; Score 67; DB 2; Length 3792;  
Best Local Similarity 100.0%; Pred. No. 2e-14;  
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 GTGATCCCGGGGCTGACGAATTCATATCCCTGACCTCGAGG 110  
DB 3541 GTGATCCCGGGGCTGACGAATTCATATCCCTGACCTCGAGG 3482  
OY 111 GGGGGCC 117  
DB 3481 GGGGGCC 3475

## RESULT 15

US-08-302-752-1/c  
Sequence 1, Application US/08302752

Patent No. 6025190



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; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: THERMOSENSIBLE PLASMID
; NUMBER OF SEQUENCES: 3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentia Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,752
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9203034
; FILING DATE: 13-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO FR/93/00248
; FILING DATE: 12-MAR-1993
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3792 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-302-752-1

Query Match          44.7%; Score 67; DB 3; Length 3792;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GTGGATCCCCGGGCGCTGCAGATTGATCAAGCTATACGATACCGTCGACCTCGAGG 110
    |||||||
Db 3541 GTGGATCCCCGGGCGCTGCAGATTGATCAAGCTATACGATACCGTCGACCTCGAGG 110
    |||||||
QY 111 GGGGGCC 117
    |||||||
Db 3481 GGGGGCC 3475
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Search completed: November 10, 2002, 08:36:21  
Job time : 39.4558 secs

